SEQUENCE' LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

Goodearl, Andrew Stroobant, Paul Minghetti, Luisa Waterfield, Michael Marchionni, Mark dhen, Mario Hiles, Ian

(ii) TITLE OF INVENTION:

GLIAL MITOGENIC FACTORS, THEIR PREPARATION AND USE

(iii) NUMBER OF SEQUENCES:

189

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:

Clark & Elbing LLP 17d Federal Street

(B) STREET:

Boston

(C) CITY: (D) STATE:

Massachusetts, U.S.A. 02110

(E) COUNTRY:

(F) ZIP:

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE:

3.5" D+Ckette, 1.44 Mb IBM Compatible Pentium

(B) COMPUTER:

(vi) CURRENT APPLICATION DATA:

Windows95

(C) OPERATING SYSTEM:

FastSeq Version 2.0

(D) SOFTWARE:

(A) APPLICATION NUMBER: 08/736 019

(B) FILING DATE:

22-OCT-1996

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/471,833

(B) FILING DATE:

06-JUN-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/036,555

(B) FILING DATE:

24-MAR-199B

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/965,173

(B) FILING DATE:

23-OCT-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/907,138

(B) FILING DATE:

30-JUN-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/940,389

(B) FILING DATE:

03-SEP-1992

101

(vii) PRIOR APPLICATION DATA:

(vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: UK 91 07566.3 (B) FILING DATE: 10-APR-1991 (viii) ATTORNEY/AGENT INFORMATION: (A) NAME: (B) REGISTRATION NUMBER: 39,109 (C) REFERENCE/DOCKET NUMBER: 04585/00200Q (ix) TELECOMMUNICATION INFORMATION: (A) TELEPHONE: (B) TELEFAX: (C) TELEX: (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 1: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: Phe Lys Gly Asp Ala His Thr Glu 1 5 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine of Arginine; Xaa in position 12 is unknown.	
(B) FILING DATE: 10-APR-1991 (viii) ATTORNEY/AGENT INFORMATION: (A) NAME: Bieker-Brady, Kristina 39,109 (C) REFERENCE/DOCKET NUMBER: 04585/00200Q (ix) TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 617) 428-0200 (B) TELEFAX: 617) 428-7045 (C) TELEX: (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 1: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 8 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: Phe Lys Gly Asp Ala His Thr Glu 1 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine of the content	
(A) NAME: (B) REGISTRATION NUMBER: 39,109 (C) REFERENCE/DOCKET NUMBER: 04585/00200Q (ix) TELECOMMUNICATION INFORMATION: (A) TELEPHONE: (B) TELEFAX: (C) TELEX: (C) TELEX: (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 1: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: (XI) SEQUENCE DESCRIPTION: SEQ ID NO: 1: Phe Lys Gly Asp Ala His Thr Glu 1 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: (D) OTHER INFORMATION: Xaa in position 1 is Lysine of	
(B) REGISTRATION NUMBER: 39,109 (C) REFERENCE/DOCKET NUMBER: 04585/00200Q (ix) TELECOMMUNICATION INFORMATION: (A) TELEPHONE: (617) 428-0200 (B) TELEFAX: (617) 428-7045 (C) TELEX: (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 1: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 8 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: Phe Lys Gly Asp Ala His Thr Glu 1 5 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine of	
(A) TELEPHONE: (B) TELEFAX: (C) TELEX: (C) TELEX: (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: (D) TOPOLOGY: (E) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: (C) STRANDEDNESS: (D) TOPOLOGY: (E) NO: 1: (I) SEQUENCE DESCRIPTION: SEQ ID NO: 1: (I) SEQUENCE CHARACTERISTICS: (I) SEQUENCE CHARACTERISTICS: (II) SEQUENCE CHARACTERISTICS: (III) SEQUENCE CHARACT	
(B) TELEFAX: (C) TELEX: (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 1: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: Phe Lys Gly Asp Ala His Thr Glu 1 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine of	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: Phe Lys Gly Asp Ala His Thr Glu 1 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine of	
(A) LENGTH: 8 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: Phe Lys Gly Asp Ala His Thr Glu 1 5 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine of	
(B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: Phe Lys Gly Asp Ala His Thr Glu 1 5 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine of	
Phe Lys Gly Asp Ala His Thr Glu (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine of	
1 5 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine of	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine of	
(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine of	
(B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine of	
(D) OTHER INFORMATION: Xaa in position 1 is Lysine of	
(D) OTHER INFORMATION: Xaa in position 1 is Lysine of Arginine; Xaa in position 12 is unknown.	
ì	or
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
Xaa Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys	
1 5 10	
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 3:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 12 (B) TYPE: amino acid (C) STRANDEDNESS:	

	(D) TOPOLOGY: linear			
	(ix) FEATURE:			
Argi	(D) OTHER INFORMATION: Xaa in inine; Xaa in position 10 is unknown.	position 1 is	Lysine or	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO	3:		
Xaa 1	Thr Glu Thr Ser Ser Ser Gly Leu Xaa 5 10	Leu Lys		
(2)	INFORMATION FOR SEQUENCE IDENTIFICAT	IDN NUMBER:	4:	·
	(i) SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 9 (B) TYPE: amino (C) STRANDEDNESS: (D) TOPOLOGY: linear			
	(ix) FEATURE:			
	(D) OTHER INFORMATION: Xaa in	position 1 is	Lysine or	Arginine.
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO	: 4:		
Xaa 1	Lys Leu Gly Glu Met Trp Ala Glu 5			
(2)	INFORMATION FOR SEQUENCE IDENTIFICAT	ION NUMBER:	5:	
	(i) SEQUENCE CHARACTERISTICS:	0		
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: amino linear	acid		
	(ix) FEATURE:			
	(D) OTHER INFORMATION: Xaa in	posi tio n 1 is	Lysine or	Arginine.
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO	: 5:		
Xaa 1	Leu Gly Glu Lys Arg Ala 5			
(2)	INFORMATION FOR SEQUENCE IDENTIFICAT	ION NUMBER:	6:	
	(i) SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 15 (B) TYPE: amino (C) STRANDEDNESS: (D) TOPOLOGY: linear			
	(ix) FEATURE:			
	(D) OTHER INFORMATION: Xaa in	position 1 is	Lysine or	Arginine.
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO	: 6:		

>

Xaa	Ile Lys Ser Glu His Ala Gly Leu Ser Ile Gly Asp Thr Ala Lys
1	5 10 / 15
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 7:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 13 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear
	(ix) FEATURE:
	(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO 7:
Xaa	Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
1	5 19
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 8:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: (ix) FEATURE:
	(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
Xaa 1	Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys 5 10 15
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 9:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: 13 amino acid linear
	(ix) FEATURE:
Argi	(D) OTHER INFORMATION: Xaa in position 1 is Lysine or nine and Xaa in position 12 is unknown.
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
Xaa	Met Ser Glu Tyr Ala Phe Phe Val Gln Thr Xaa Arg
1	5 10

<i>i</i> = <i>i</i>			
(2)	INFORMATION FOR SEQUENCE IDEN		10:
	(i) SEQUENCE CHARACTERISTICS:	,	
	(A) LENGTH: (B) TYPE:	14 amino acid	
	(C) STRANDEDNESS:		
	(D) TOPOLOGY:	linear	
	(ix) FEATURE:		
	(D) OTHER INFORMATION:	Xaa in position 1 is	Lysine or Arginine.
	(xi) SEQUENCÈ DESCRIPTION: SE	Q ID NO: 10:	
Xaa	Ser Glu His Pro Gly Leu Ser I	le Gly Asp thr Ala Ly	s
1	5	10	
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	11:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH:	10/	
	(B) TYPE: (C) STRANDEDNESS:	amino acid	
	(D) TOPOLOGY:	finear	
	(ix) FEATURE:		
Arg	(D) OTHER INFORMATION inine; Xaa in position 8 is un	Xaa in position 1 is	Lysine or
	(xi) SEQUENCE DESCRIPTION SE	Q ID NO: 11:	
Xaa	Ala Gly Tyr Phe Ala Glu Xaa A	ala Arg	
1	5 //	10	
	V		
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	12:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH:	9	
	(B) TYPE: (C) STRANDEDNESS:	amino acid	
	(D) TOPOLOGY:	linear	
	(ix) FEATURE:		
Arg:	(D) OTHER INFORMATION: inine; Xaa in position 7 is un	Xaa in position 1 is known.	Lysine or
	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 12:	
Xaa 1	Lys Leu Glu Phe Leu Xaa Ala I	ys	
,	/		
(2)	INFORMATION FOR SEQUENCE IDEN		13:
	(i) SEQUENCE CHARACTERISTICS:		
	1		

		(B)	LENGTH: TYPE:	11 amino acid					
			STRANDEDNESS: TOPOLOGY:	linear					
	(ix)	FEAT	TURE:	,	/				
		(D)	OTHER INFORMATION:	Xaa in position 1 is	Lysine or	Arginine.			
	(xi)	SEQU	JENCE DESCRIPTION: SE	Q ID NO: 13:					
Xaa	Thr T	hr (Glu Met Ala Ser Glu G	ln Gly Ala					
1			5	10					
(2)	INFOR	TAM	ION FOR SEQUENCE IDEN	TIFICATION NUMBER:	14:				
	(i) S	EQUE	ENCE CHARACTERISTICS:	/ .					
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	10 amino acid lingar		a.			
	(ix)	FEAT	rure:	$\stackrel{\checkmark}{\sim}$					
		(D)	OTHER INFORMATION	Xaa in position 1 is	Lysine or	Arginine.			
	(xi)	SEQU	JENCE DESCRIPTION: SE	Q ID NO: 14:					
Xaa	Ala I	ys C	Glu Ala Leu Ala Ala L	eu Lys					
1			5	10					
(2)	INFOR	TAMS	ION FOR SEQUENCE IDEN	TIFICATION NUMBER:	15:				
	(i) S	EQUE	ENCE CHARACTERISTICS:						
		(B) (C)	LENGTH: TYPE: STRANDEDNESS:	8 amino acid					
			TOPOLOGY:/	linear					
	(ix)		/						
		(D)	OTHER/INFORMATION:	Lysine or	Arginine.				
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:								
Xaa 1	Phe V	al I	Leu ¢ln Ala Lys Lys 5						
(2)	INFOR	TAMS	19N FOR SEQUENCE IDEN	TIFICATION NUMBER:	16:				
	(i) S	EQUE	/ ENCE CHARACTERISTICS:						
		(A) (B)	LENGTH: TYPE: STRANDEDNESS:	6 amino acid					
		ζ <u>Б</u> ;	TOPOLOGY:	linear					

	(ix) FEATURE:		
	(D) OTHER INFORMATION:	Xaa in position 1 is Lysine o	Arginine
	(xi) SEQUENCE DESCRIPTION: SEQ	Q ID NO: 16:	,
Xaa 1	Leu Gly Glu Met Trp 5		
(2)	INFORMATION FOR SEQUENCE IDENT	CIFICATION NUMBER: 17:	
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	16 amino acid linear	
	(xi) SEQUENCE DESCRIPTION: SEQ	Q ID NO: 17:/	
Glu 1	Tyr Lys Cys Leu Lys Phe Lys Tr 5	rp Phe Lys Lys Ala Thr Val Met 10 15	
(2)	INFORMATION FOR SEQUENCE IDENT	CIFICATION NUMBER: 18:	
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	10 amino acid linear	
	(ix) FEATURE: (D) OTHER INFORMATION:	Xaa in position 8 is unknown.	
	(xi) SEQUENCE DESCRIPTION: SEQ	Q ID NO: 18:	
Glu 1	Ala Lys Tyr Phe Ser Lys Xaa As		
(2)	INFORMATION FOR SEQUENCE IDENT	rification number: 19:	
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	7 amino acid linear	
	(ix) FEATURE:		
	(D) OTHER INFORMATION:	Xaa in position 2 is unknown.	
	(xi) SEQUENCE DESCRIPTION: SEQ	Q ID NO: 19:	
Glu 1	Xaa Lys Phe Tyr Val Pro		

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 20:						
(i) SEQUENCE CHARACTERISTICS:						
(A) LENGTH: 26 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear						
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:						
Glu Leu Ser Phe Ala Ser Val Arg Leu Pro Gly Cys Pro Pro Gly Val						
Asp Pro Met Val Ser Phe Pro Val Ala Leu 20 25						
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 21:						
(i) SEQUENCE CHARACTERISTICS:						
(A) LENGTH: 2003 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear						
(ix) FEATURE:						
(D) OTHER INFORMATION: N in positions 31 and 32 could be either A or G.						
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:						
GGAATTCCTT TTTTTTTTT TTTTTTTTTTTTTTTTTTT	60					
TTTCTGTGGT TCCATCCACT TCTTCCCCCT CCTCCTCCCA TAAACAACTC TCCTACCCCT 1						
GCACCCCAA TAAATAAATA AAAGGAGGAG GGCAAGGGGG GAGGAGGAGG AGTGGTGCTG	180					
CGAGGGGAAG GAAAAGGGAG GCGCGAG AAGAGCCGGG CAGAGTCCGA ACCGACAGCC 2						
AGAAGCCCGC ACGCACCTCG CACC ATG AGA TGG CGA CGC GCC CCG CGC Met Arg Trp Arg Ala Pro Arg Arg 1	291					
TCC GGG CGT CCC GGC CCC CGG GCC CAG CGC CCC GGC TCC GCC GCC CGC Ser Gly Arg Pro Gly Pro Arg Ala Gln Arg Pro Gly Ser Ala Ala Arg 10 15 20 25	339					
TCG TCG CCG CCG CTG CCG CTG CCA CTA CTG CTG CTG GGG ACC Ser Ser Pro Pro Leu Pro Leu Leu Leu Leu Leu Leu Gly Thr 30 35 40	387					
GCG GCC CTG CCG GGG GCG GCG GCC GGC AAC GAG GCG GC	435					
GGG GCC TCG GTG TGC TAC TCG TCC CCG CCC AGC GTG GGA TCG GTG CAG Gly Ala Ser Val Cys Tyr Ser Ser Pro Pro Ser Val Gly Ser Val Gln 60 65 70	483					
GAG CTA GCT CAG CGC GCC GCG GTG GTC ATC GAG GGA AAG GTG CAC CCG	531					

Glu	Leu 75	Ala	Gln	Arg	Ala	Ala 80	Val	Val	Ile	Glu	Gly 85	Lys	Val	His	Pro	/	
CAG Gln 90	CGG Arg	CGG Arg	CAG Gln	CAG Gln	GGG Gly 95	GCA Ala	CTC Leu	GAC Asp	AGG Arg	AAG Lys 100	GCG Ala	GCG Ala	GCG Ala	GCG Ala	GCG/ Al⁄a 1⁄05	/	579
					TGG Trp												627
					CCG Pro												675
					TGG Trp												723
					CCC Pro												771
					TTG Leu 175												819
GGG Gly	ACC Thr	TGG Trp	GGC Gly	CAC His 190	CCC Pro	GCC Ala	TTC Phe	CCC Pro	TCC Ser 195	TGC Cys	GGG Gly	AGG Arg	CTC Leu	AAG Lys 200	GAG Glu		867
GAC Asp	AGC Ser	AGG Arg	TAC Tyr 205	ATC Ile	TTC Phe	TTC Phe	ATG Met	GAG Glu 210	CCC Pro	GAC Asp	GCC Ala	AAC Asn	AGC Ser 215	ACC Thr	AGC Ser		915
CGC Arg	GCG Ala	CCG Pro 220	GCC Ala	GCC Ala	TTC Phe	¢GA Arg	GCC Ala 225	TCT Ser	TTC Phe	CCC Pro	CCT Pro	CTG Leu 230	GAG Glu	ACG Thr	GGC Gly		963
					GAG Glu												1011
					AAA Lys 255											٠	1059
					CGG Arg												1107
					AAG Lys												1155
					ATA Ile												1203
		AAA			CTG Leu		GAT					ATG					1251

ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val 230 245	1299/
GAA TCA AAC GCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA Glu Ser Asn Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val 250 255	1/347
AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys 265 270 275	1395
TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG TGC AAG TGC Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys 280 285 290	1443
CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser 295 300 305	1491
TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT CAA Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu 400 405 410	1530
TAGGAGCATG CTCAGTTGGT GCTGCTTTCT TGTTGCTGCA CTCCCCTCA GATTCCACCT	1590
AGAGCTAGAT GTGTCTTACC AGATCTAATA TTGACTGCCT CTGCCTGTCG CATGAGAACA	1650
TTAACAAAAG CAATTGTATT ACTTCCTCTG TTCGCGACTA GTTGGCTCTG AGATACTAAT	1710
AGGTGTGTGA GGCTCCGGAT GTTTCTGGAA TTGATATTGA ATGATGTGAT ACAAATTGAT	1770
AGTCAATATC AAGCAGTGAA ATATGATAAT AAAGGCATTT CAAAGTCTCA CTTTTATTGA	1830
TAAAATAAAA ATCATTCTAC TGAACAGTCC ATCTTCTTTA TACAATGACC ACATCCTGAA	1890
AAGGGTGTTG CTAAGCTGTA ACCGATATGC ACTTGAAATG ATGGTAAGTT AATTTTGATT	1950
CAGAATGTGT TATTTGTCAC AAATAAACAT AATAAAAGGA AAAAAAAAAA	2003

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH (B) TYPE:

12

amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

linear

(ix) FEATURE:

OTHER INFORMATION: Xaa in position 11 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys
1 10

(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	23:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: (B) TYPE:	11 amino acid	
	(C) STRANDEDNESS:	linear	,
	(D) TOPOLOGY:	Illiear	
	(ix) FEATURE:		. /
	(D) OTHER INFORMATION:	-	unknown.
	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 23:	
Thr	Glu Thr Ser Ser Ser Gly Leu X	aa Leu Lys	
1	5	10	
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	24:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH:	12	
	(B) TYPE: (C) STRANDEDNESS:	amino adid	
	(D) TOPOLOGY:	linear	
	(xi) SEQUENCE DESCRIPTION: SE		
Ala	Ser Leu Ala Asp Glu Tyr Glu T	ýr Met Arg Lys	
1	5	10	
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	25:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH:	9	
	(B) TYPE: (C) STRANDEDNESS:	amino acid	
	(D) TOPOLOGY:	linear	
	(ix) FEATURE:		
	(D) OTHER INFORMATION:	Xaa in position 7 is	unknown.
	(xi) SEQUENCE DESCRIPTION: SE	O TD NO. 25.	
	(XI) SEQUENCE DESCRIPTION: SE	Q 1D NO. 25.	
Ala 1	Gly Tyr Phe Ala Glu Xaa Ala A		
1	Gly Tyr Phe Ala Glu Xaa Ala A	rg	26.
_	Gly Tyr Phe Ala Glu Xaa Ala A 5 INFORMATION FOR SEQUENCE IDEN	rg TIFICATION NUMBER:	26:
1	Gly Tyr Phe Ala Glu Xaa Ala A 5 INFORMATION FOR SEQUENCE IDEN (i) SEQUENCE CHARACTERISTICS:	rg TIFICATION NUMBER:	26:
1	Gly Tyr Phe Ala Glu Xaa Ala A 5 INFORMATION FOR SEQUENCE IDEN (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE:	rg TIFICATION NUMBER:	26:
1	Gly Tyr Phe Ala Glu Xaa Ala A 5 INFORMATION FOR SEQUENCE IDEN (i) SEQUENCE CHARACTERISTICS: (A) LENGTH:	rg TIFICATION NUMBER:	26:

	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 26:	
Thr	Thr Glu Met Ala Ser Glu Gln G	ly Ala	
1	5	10	
>		THE CAMEAN AND ED	27 -
(2)	INFORMATION FOR SEQUENCE IDEN		27:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS:	9 amino acid	
	(D) TOPOLOGY:	linear	
	(xi) SEQUENCE DESCRIPTION: SE	,	
Ala 1	Lys Glu Ala Leu Ala Ala Leu L 5	yys	
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER	28:
(2)	(i) SEQUENCE CHARACTERISTICS:		201
	(A) LENGTH:	7	
	(B) TYPE: (C) STRANDEDNESS:	amino acid	
	(D) TOPOLOGY:	linear	
	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 28:	
Phe 1	Val Leu Gln Ala Lys Lys 5		
_	/		
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	29:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: (B) TYPE:	21 amino acid	
	(C) STRANDEDNESS: (D) TOPOLOGY:	linear	
	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 29:	
Glu	Thr Gln Pro Asp Pro Gly Gln I	le Leu Lys Lys Val Pr	o Met Val
1	5/	10	15
Ile	Gly Ala Tyr Thr		
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	30:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH:	21	
	(B) TYPE: (C) STRANDEDNESS:	amino acid	
	(D) TOPOLOGY:	linear	

	(ix)	FEA'	TURE:							
unkr	own.	(D)	OTHER	INFORMATI	ON:	Xaa :	in positi	lons 1,	3, 17	and 19 is
	(xi)	SEQ	UENCE DI	ESCRIPTION	: SEÇ	ID I	NO: 30:			
Xaa 1	Glu	Xaa 1	Lys Glu 5	Gly Arg G	ly Ly	s Gl		/ Lys L	ys Lys 15	Glu
Xaa	Gly	Xaa (Gly Lys 20							
(2)	INFO	RMAT	ION FOR	SEQUENCE	IDENT	TIFIC	ATION NUM	BER:	31:/	/
	(i)	SEQU	ENCE CH	ARACTERIST	CICS:					
		(B)	LENGTH TYPE:			13 amin	o acid	/		
			TOPOLO			line	ar			
	(xi)	SEQ	UENCE D	ESCRIPTION	: SEÇ) ID I	NO: 31:			
Ala 1	Glu	Lys (Glu Lys 5	Thr Phe C	ys Va	al As: 1		/ Glu		
(2)	INFO	ORMAT:	ION FOR	SEQUENCE	IDENT	TIFIC.	ATION NUM	MBER:	32:	
	(i)	SEQU	ENCE CH	ARACTERIST	CICS:	/				
		(B) (C)	LENGTH TYPE: STRANDI TOPOLOG	EDNESS:	/	8 amin line	o acid ar			
	(ix)	FEA'	TURE:							
		(D)	OTHER	INFORMAT	ON:	Xaa	in positi	ion 6 i	s unkno	wn.
	(xi)	SEQ	UENCE D	ESCRIPTION	: SEÇ	O ID	NO: 32:			
Lys 1	Leu	Glu i	Phe Leu 5	Xaa Ala I	ys					
				,						
(2)				SEQUENCE		TIFIC	ATION NUM	MBER:	33:	
	(i)	SEQU	ENCE CH	ARACTERIST	ICS:					
		(A) (B) (C) (D)	TYPE:	EDNESS:		9 amin line	o acid ar			
	(ix)	FEA	TURE:							
Arai	inine	(D)	OTHER	INFORMATI	ON: X	Kaa i	n positio	on 1 is	Lysine	or

	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO: 33:
Xaa 1	a Val His Gln Val Trp Ala Ala Lys	
		
(2)	INFORMATION FOR SEQUENCE IDENTIF	FICATION NUMBER: 34:
	(i) SEQUENCE CHARACTERISTICS:	
	(C) STRANDEDNESS:	inear
	(ix) FEATURE:	
Arg	(D) OTHER INFORMATION: Xaa gininel; Xaa in position 11 is unl	a in position 1 is Lysine or known.
	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO: 34:
Xaa	a Tyr Ile Phe Phe Met Glu Pro Glu	Ala Xaa Ser Ser Gly
1	5	10/
(2)) INFORMATION FOR SEQUENCE IDENTI	FICATION NUMBER: 35:
	(i) SEQUENCE CHARACTERISTICS:	
	/_	1
	(B) TYPE: ar	mino acid
	(b) lorollogi.	, ,
	(ix) FEATURE:	
Arg:	(D) OTHER INFORMATION: Xaa ginine; Xaa in position 13 is unki	a in position 1 is Lysine or nown.
	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO: 35:
Xaa	a Leu Gly Ala Trp Gly Pro Pro Ala	Phe Pro Val Xaa Tyr
1	1 /5	10
(2)) INFORMATION FOR SEQUENCE IDENTI:	FICATION NUMBER: 36:
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 9 (B) TYPE: an (C) STRANDEDNESS:	mino acid
		inear
	(1x) FEATURE:	
Arg	(D) OTHER INFORMATION: Xao	a in position 1 is Lysine or
	(xi) SEQUENCE DESCRIPTION: SEQ	TD NO: 36:

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 37: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37: Xaa Ala Ser Pro Val Ser Val Gly Ser Val Gln Gly Leu Val Gln Arg (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 38: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: ∕amino acid (C) STRANDEDNESS:
(D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38: Xaa Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr 1 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 39: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine; Xaa in position 6 is unknown. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39: Xaa Asp Leu Leu Leu Xaa Val

Xaa Trp Phe Val Val Ile Glu Gly Lys

(2)	INFORMAT	ON FOR	SEQUENCE	IDENT	FICATI	ON NUI	MBER:	4	0:		
	(i) SEQU	ENCE CHA	ARACTERIS	TICS:							/
	1 1	LENGTH:	:		39 amino a	aid					
	(C)	TYPE:				cia					
	(D)	TOPOLOG	3Y:	•	linear						
	(1)				TD 170						
			ESCRIPTIO					. /			
Cys 1	Thr Cys	Gly Cys 5	Cys Lys	Cys Cys	Arg T	hr Th	r Cys	Ala(Cys 15	Arg	
Cys	Ala Gly	Ala Ala 20	Gly Gly	Thr Cys		hr Cys	s That	Cys (Cys	Thr	
Thr	Cys Thr 35	Cys Ala	Gly Cys		-						
(2)	INFORMAT	ION FOR	SEQUENCE	IDENT	FICATI	ON NUI	MBER:	4:	1:		
	(i) SEQU	ENCE CHA	ARACTERIS	TICS:							
	(B) (C)	LENGTH: TYPE: STRANDE	EDNESS:		24/ mino a inear	cid					
	(xi) SEO	UENCE DE	ESCRIPTIO	N: SEO	ID NO:	41:					
_		Cys Gly	Cys Thr		Thr T		s Thr	Thr		Thr	
1	a.] a	5		-	10				15		
Tnr	GIY Cys	Cys Cys 20	Thr Thr	Cys							
(2)	INFORMAT	'ION FOR	SEQUENCE	IDENT	FICATI	ON NU	MBER:	4:	2:		
	(i) SEQU	ENCE CHA	ARACTERIS	TICS:							
	(B)	/STRANDE	EDNESS:	1	50 nucleic single .inear	acid					
	(xi) SEQ	UENCE DE	ESCRIPTIO	N: SEQ	ID NO:	42:					
AAG1	rgcccaa a	TGAGTTT	AC TGGTGA	TCGC TO	CCAAAA	CT AC	GTAAT(GGC C	AGCI	TCTAC	60
(2)/	INFORMAT	ION FOR	SEQUENCE	IDENT	FICATI	ON NUI	MBER:	4:	3:		
	(i) SEQU	ENCE CHA	ARACTERIS	TICS:							
/	(B) (C)	LENGTH: TYPE: STRANDE TOPOLOG	EDNESS:	1	86 nucleic single linear	acid					

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43: 36 AGTACGTCCA CTCCCTTTCT GTCTCTGCCT GAATAG (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 44: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44: AAGGCGGAGG AGCTGTACCA GAAGAGAGTG CTGACCATAA CCGGCAT/CTG CATCGCCCTC 60 CTTGTGGTCG GCATCATGTG TGTGGTGGCC TACTGCAAAA CCAAGAAACA GCGGAAAAAG 120 CTGCATGACC GTCTTCGGCA GAGCCTTCGG TCTGAACGAA AQAATATGAT GAACATTGCC 180 AATGGGCCTC ACCATCCTAA CCCACCCCC GAGAATGTCC/AGCTGGTGAA TCAATACGTA 240 TCTAAAAACG TCATCTCCAG TGAGCATATT GTTGAGAGÁG AAGCAGAGAC ATCCTTTTCC 300 ACCAGTCACT ATACTTCCAC AGCCCATCAC TCCACTACTG TCACCCAGAC TCCTAGCCAC 360 AGCTGGAGCA ACGGACACAC TGAAAGCATC CTTTCCGAAA GCCACTCTGT AATCGTGATG 420 TCATCCGTAG AAAACAGTAG GCACAGCAGC ÇCAACTGGGG GCCCAAGAGG ACGTCTTAAT 480 GGCACAGGAG GCCCTCGTGA ATGTAACAGO TTCCTCAGGC ATGCCAGAGA AACCCCTGAT 540 TCCTACCGAG ACTCTCCTCA TAGTGAAAG 569 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 45: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: amino acid (C) STRANDÉDNESS: (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45: Val His Gln ∜al Trp Ala Ala Lys 1 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 46: SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acid (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 10 is unknown.

	(xi) SEQ	JENCE DESCRIPTION	SEQ ID NO: 46:	
Tyr 1	Ile Phe	Phe Met Glu Pro (5	lu Ala Xaa Ser Ser Gly 10	
(2)	INFORMAT	ION FOR SEQUENCE	IDENTIFICATION NUMBER:	47:
	(i) SEQU	ENCE CHARACTERIS	CS:	
	(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	13 amino acid linear	
	(ix) FEA	TURE:		
	(D)	OTHER INFORMAT	ON: Xaa in position 12	is unknown.
	(xi) SEQ	UENCE DESCRIPTION	: SEQ ID NO: 47:	
Leu 1	Gly Ala '	Trp Gly Pro Pro 5	la Phe Pro Val Xaa Tyr 10	
(2)	INFORMAT	ION FOR SEQUENCE	IDENTIFICATION NUMBER:	48:
	(i) SEQU	ENCE CHARACTERIS	ics.	
	(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	8 amino acid linear	
	(xi) SEQ	UENCE DESCRIPTIO	: SEQ ID NO: 48:	
Trp 1	Phe Val	Val Ile Gly Gly 5	ys	
(2)	INFORMAT	ION FOR SEQUENCE	IDENTIFICATION NUMBER:	49:
	(i) SEQU	ENCE CHARACTERIS	ICS:	
	(A) (B) (C) (D)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	15 amino acid linear	
	. /	UENCE DESCRIPTIO		
Ala 1			er Val Gln Glu Leu Val (10	Gln Arg 15
(2)	INFORMAT	TON FOR SPOTENCE	IDENTIFICATION NUMBER:	50:
1/	/	ENCE CHARACTERIS		50.
	(B) (C)	LENGTH: TYPE: STRANDEDNESS:	12 amino acid	
	(ע)	TOPOLOGY:	linear	

	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 50:
Val 1	Cys Leu Leu Thr Val Ala Ala I 5	eu Pro Pro Thr
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER: 51:
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	9 amino acid linear
	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 51:
Lys 1	Val His Gln Val Trp Ala Ala I 5	bys
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER: 52:
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	13 amino acid linear
	(ix) FEATURE:	
	(d) OTHER INFORMATION:	Xaa in position 12 is unknown.
	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 52:
Lys 1	Ala Ser Leu Ala Asp Ser Gly G	Glu Tyr Met Xaa Lys 10
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER: 53:
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH:	6
	(B) TYPE; (C) STRANDEDNESS:	amino acid
	(D) TOPOLOGY:	linear
	(ix) FEATURE:	
		Xaa in position 5 is unknown.
	(xi) SÉQUENCE DESCRIPTION: SE	Q ID NO: 53:
Asp 1	Leu Leu Leu Xaa Val	
(2)/	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER: 54:
	(i) SEQUENCE CHARACTERISTICS	

		(B)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	20 nucleic single linear	acid			
	(ix)	FE	ATURE:					/
or T G or		(D) at po	OTHER INFORMATION: osition 6 is A or G;	N at posi	itions itions	3, 12 9 and	and 18 i 15 1s A,	s C T,
	(xi)	SEQ	UENCE DESCRIPTION: SE	EQ ID NO:	54:			
TTNA	ANGG	NG AI	NGCNCANAC					20
(2)	INFO	RMAT:	ION FOR SEQUENCE IDEN	TIFICATIO	ом ицин	/ BER:	55:	
	(i) :	SEQUI	ENCE CHARACTERISTICS:	:				
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	21 nucleic single linear	acid			
	(ix)	FE	ATURE:					
N at		(D) itio	OTHER INFORMATION:	N at pos or G; N	sitions at pos	s 7 and sition	13 is C 19 is A,	or T;
	(xi)	SEQ	JENCE DESCRIPTION: SE	EQ ID NO:	55:			
CATN	TANT	CN TA	ANTCNTCNG C					21
(2)			ION FOR SEQUENCE IDEN		ON NUME	BER:	56:	
	(1)	-	ENCE CHARACTERISTICS					
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	20 nucleic single linear	acid			
	(ix)	FE	ATURE:					
N at	pos	(D)	OTHER INFORMATION: OS 6, 9, and 18 is A,	N at pos T, G or	sitions C.	3 and	15 is C	or T
	(xi)	SEQ	UENCE DESCRIPTION: SE	EQ ID NO:	56:			
TGNT	'CNGAI	MG CO	CATNTCNGT					20
(2)	INFO	RMAT:	ION FOR SEQUENCE IDEN	TIFICATIO	AMUM NC	BER:	57:	
,	(i) :	SEQUI	ENCE CHARACTERISTICS	:				
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	20 nucleic single linear	acid			

	(ix)	FE	ATURE:		
N at	posi	(D) Ltio	OTHER INFORMATION n 6 is A or G; N at	: N at positions 3 and 14 is C or T positions 9 and 17 is A, T, G or C	: ;
	(xi)	SEQ	UENCE DESCRIPTION:	SEQ ID NO: 57:	
TGNT	CNCTI	1G C	CATNTCNGT	20/	/
(2)	INFOR	TAMS:	ION FOR SEQUENCE ID	ENTIFICATION NUMBER: 58:	
	(i) S	SEQUI	ENCE CHARACTERISTIC	s:	
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	20 nucleic acid single linear	
	(ix)	FE	ATURE:		
at p G or		(D) ion	OTHER INFORMATION 18 is C or T; N at	: N at position 3 is A, G or T; N positions 6, 12, and 15 is A, T,	
	(xi)	SEQ	UENCE DESCRIPTION:	SEQ ID NO: 58:	
CCNA	TNAC	CA TI	NGGNACNTT	20	
(2)	INFO	RMAT	ION FOR SEQUENCE ID	ENTIFICATION NUMBER: 59:	
	(i) S	EQU!	ENCE CHARACTERISTIC	s:/	
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	20 nucleic acid single linear	
	(ix)	FE	ATURE:		
posi	tion	(D) 15	OTHER INFORMATION is A or G; N at pos	: N at position 12 is C or T; N at itions 3, 9 and 18 is A, T, G or C.	
	(xi)	SEQ	UENCE DESCRIPTION:	SEQ ID NO: 59:	
GCNG	CCCAI	VA C	YTGRTGNAC	20	
(2)	INFO	RMAT	ION FOR SEQUENCE ID	ENTIFICATION NUMBER: 60:	
	(i) S	SEQU:	ence Characteristic	S:	
		(A) (B) (Q) (D)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	20 nucleic acid single linear	
	(ix)	FE.	ATURE:		
N at	pos:	(D)	OTHER INFORMATION ns 5 and 8 is A or	: N at positions 3 and 9 is C or TG; N at position 6 is A, T, G or C.	7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

20 GCNTCNGGNT CCATNAANAA (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 61: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 (B) TYPE: nucleic acid single (C) STRANDEDNESS: linear (D) TOPOLOGY: (ix) FEATURE: (D) OTHER INFORMATION: N at position 6 is A/G or T; N at position 3 is C or T; N at position 15 is A or G; N at positions 9 and 11 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61: 20 CCNTCNATNA CNACNAACCA (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 62: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 (B) TYPE: nuclei¢ acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N at positions 6 and 9 is A or G; N at positions 3, 11 and 14 is A/T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62: 17 TCNGCNAANT ANCCNGC (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 63: (i) SEQUENCE CHARACTÉRISTICS: (A) LENGTH: 20 (B) TYPE: nucleic acid (C) STRANDEONESS: single (D) TOPOLOGY: linear (ix) FEATURE/ OTHER INFORMATION: N at positions 12 and 15 is C or T; N at positions/3, 6, 9 and 17 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63: GCNGCNAGNG/CNTCNTTNGC 20 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 64: SEQUENCE CHARACTERISTICS:

(A) LENGTH: (B) TYPE: nucleic acid (C) STRANDEDNESS: single linear (D) TOPOLOGY: (ix) FEATURE: (D) OTHER INFORMATION: N at positions 6, 12 and 15 is q'or T; N at positions 3, 9, and 18 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64: 20 GCNGCNAANG CNTCNTTNGC (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 nucleic acid (B) TYPE: (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N at positions 3 and 9 is C or T; N at position 18 is A or G; N at positions 6, 12 and 15 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65: 20 TTNTTNGCNT GNAGNACNAA (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 66: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 (B) TYPE: nucleic acid (C) STRANDEDNESS single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N at positions 3, 9 and 12 is C or T; N at position 18 is A or G; N at positions 6 and 15 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66: TTNTTNGCNT GNAANACNAA 20 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear FEATURE: (ix/)

(D) OTHER INFORMATION: N at positions 9 and 12 is C or T; N at positions 3, 6 and 15 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67: 17 TGNACNAGNT CNTGNAC (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 68: (i) SEQUENCE CHARACTERISTICS: 17 . (A) LENGTH: (B) TYPE: (C) STRANDEDNESS: nucleic acid single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N at positions 6, 9, and 12 is C or T; N at positions 3 and 15 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: \$8: TGNACNAANT CNTGNAC 17 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 69: (i) SEQUENCE CHARACTERISTICS: 21 (A) LENGTH: (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N at position 7 is C or T; N at positions 4 and 16 is A or G; N at positions 10, 13 and 19 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69: CATNTANTON CONGANTONG C 21 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 70: (i) SEQUENCE CHARACTERISTICS: LENGTH: 21 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix/) FEATURE: (D) OTHER INFORMATION: N at position 7 is C or T; N at positions 4, 13 and 16 is A or G; N at positions 10 and 19 is A, T, & or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

(2)	INFOR	RMAT]	ION FOR	SEQUENCE	E IDEN	rificatio	ON NUME	BER:	71:	
	(i) S	EQUE	ENCE CHA	RACTERIS	STICS:					
		(B) (C)	LENGTH: TYPE: STRANDE TOPOLOG	DNESS:		21 nucleic single linear	acid			/
	(ix)	FE <i>I</i>	ATURE:						/	
N at G or		(D) Ltion	OTHER n 4 is A	INFORMAT or G; 1	TION: 1 N at po	N at pos ositions	itions 1, 7,	10 and 13 and	19 is 16 is	C or T;
	(xi)	SEQU	JENCE DE	SCRIPTIO	ON: SE	Q ID NO:	71:/			
NGAN	TCNGC	CN A	ANGANGCN	IT T						21
(2)	TNFOE	РМДТ ⁻	ION FOR	SEQUENCI	E IDEN'	rificayi	/ ON NUME	BER:	72:	
(2)				RACTERIS						
	(1)		LENGTH:			21				
		(B)	TYPE: STRANDE	DNESS:	/	nucleic single linear	acid			
	(ix)	FE?	ATURE:							
posi G oi		(D) 4 is	OTHER s A or G	INFORMA ; N at]	PION: 1 positio	N at posons 1, 7	ition 1 , 10, 1	19 is C 13 and	or T; 16 is	N at A, T,
	(xi)	SEQU	JENCE DE	ESCRIPTIO	ON: SE	Q ID NO:	72:			
NGAI	TCNGC	CN AC	GNGANGC	yr T						21
(0)							011 1HB47			
(2)						rificati:	ON NUME	BER:	73:	
	(1) 8			RACTERI	STICS:					
		(A) (B)/ (C) (D)	LENGTH: TYPE: STRANDE TOPOLOG	EDNESS:		21 nucleic single linear	acid			
	(ix)/	FEA	ATURE:							
	posi		OTHER ns 1 and	INFORMA' 1 4 is A	FION: 1 or G;	N at pos N at po	itions sitions	10 and 3 7, 13	19 is and 1	C or T, 6 is A,
	(xi)	SEQ	UENCE DE	ESCRIPTIO	ON: SE	Q ID NO:	73:			
NCTI	NTCNGO	CN A	ANGANGCI	T T						21
(2)	INFOR	RMAT:	ION FOR	SEQUENC	E IDEN'	TIFICATI	ON NUME	BER:	74:	

(i) SEQUENCE CHARACTERISTICS:							
(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	21 nucleic acid single linear						
(ix) FEATURE:							
(D) OTHER INFORMATION: No positions 1 and 14 is A or G; N at A, T, G or C.	at position 19 is C or 7; N at positions 7, 10, 13 and 16 is						
(xi) SEQUENCE DESCRIPTION: SEQ	Q ID NO: 74:						
NCTNTCNGCN AGNGANGCNT T	21						
(2) INFORMATION FOR SEQUENCE IDENT	rification number: 75:						
(i) SEQUENCE CHARACTERISTICS:							
	21 nucleic acid single linear						
(ix) FEATURE:							
(D) OTHER INFORMATION: N N at positions 4 and 13 is A or G, A, T, G or C.	A at positions 10 and 19 is C or T; N at positions 1, 7 and 16 is						
(xi) SEQUENCE DESCRIPTION: SEQ	Q ID NO: 75:						
NGANTCNGCN AANCTNGCNT T	21						
(2) INFORMATION FOR SEQUENCE IDENT	TIFICATION NUMBER: 76:						
(i) SEQUENCE CHARACTERISTICS:	•						
(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	21 nucleic acid single linear						
(ix) FEATURE:							
(D) OTHER INFORMATION: positions 4 and 13 is A or G; N at A, T, G or 9.	N at position 19 is C or T; N at positions 1, 7, 10 and 16 is						
(xi) SEQUENCE DESCRIPTION: SEC	Q ID NO: 76:						
NGANTCNCCN AGNCTNGCNT T 21							
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 77:							
(i) SEQUENCE CHARACTERISTICS:							
(A) LENGTH: (B) TYPE: (C) STRANDEDNESS:	730 nucleic acid single						

(D) TOPOLOGY:

linear

- (ix) FEATURE:
 - (D) OTHER INFORMATION:
- GTATGTGTCA GCCATGACCA CCCCGGCTCG TATGTCACCT GTAGATTTCC ACACGCCAAG 60
 CTCCCCCAAA TCGCCCCTT CGGAAATGTC TCCACCCGTG TCCAGCATGA CGGTGTCCAT 120
 GCCTTCCATG GCGGTCAGCC CCTTCATGGA AGAAGAGAGA CCTCTACTTC TCGTCACACC 180
 ACCAAGGCTG CGGGAGAAGA AGTTTGACCA TCACCCTCAG CAGTTCAGCT CCTTCCACCA 240
 CAACCCCGCG CATGACAGTA ACAGCCTCCC TGCTAGCCCC TTGAGGATAG TGGAGGATGA 300
 GGAGTATGAA ACGACCCAAG AGTACGAGCC AGCCCAAGAG CCTGTTAAGA AACTCGCCAA 360
 TAGCCGGCGG GCCAAAAGAA CCAAGCCCAA TGGCCACATT GCTAACAGAT TGGAAGTGGA 420
 CAGCAACACA AGCTCCCAGA GCAGTAACTC AGAGAGTGAA ACACAAGATG AAAGAGTAGG 480
 TGAAGATACG CCTTTCCTGG GCATACAGAA CCCCCTGGCA GCCAGTCTTG AGGCAACACC 540
 TGCCTTCCGC CTGGCTGACA GCAGGACTAA CCCAGCAGGC CGCTTCTCGA CACAGGAAGA 600
 AAATCCAGGCC AGGCTGTCTA GTGTAATTGC TAACCAAGAC CCTATTGCTG TATAAAACCT 660
 AAATAAACAA TTAATAAACAA 730
- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 78:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:
- 21

(B) TYPE:

- nucleic acid
- (C) STRANDEDNESS
- single
- (D) TOPOLOGY:
- linear

- (ix) FEATURE:
- (D) OTHER INFORMATION: N at positions 10 and 19 is C or T; N at positions 1, 4 and 13 is A or G; N at positions 7 and 16 is A, T, G or C.
 - (xi) SEQUENÇE DESCRIPTION: SEQ ID NO: 78:

NCTNTCNGCN AANCTNGCNT T

21

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 79:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:
- 21

(B) TYPE:

- nucleic acid
- (C) STRANDEDNESS:
- single
- (D) TOPOLOGY:
- linear

(ix) FEATURE:

	tions , G c	1,	4 and 13 is A or G; h	N at position 19 is C or T; N at N at positions 7, 10 and 16 is	/				
	(xi)	SEQ	UENCE DESCRIPTION: SEC	Q ID NO: 79:					
NCTN	CTNGC	n A	GNCTNGCNT T	21					
(2)	INFOR	TAM	ION FOR SEQUENCE IDENT	rification number: 80					
	(i) S	EQU	ENCE CHARACTERISTICS:						
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	20 nucleic acid single linear					
	(ix)	FE	ATURE:						
posi	tions	(D)	OTHER INFORMATION: 6, 17 and 18 is A, T	N at position 9 is A or G; N at , G or C.					
	(xi)	SEQ	UENCE DESCRIPTION: SEC	Q ID NO; 80:					
ACNA	.CNGAN	IA T	GGCTCNNGA	20					
(2)	INFOR	TAMS	ION FOR SEQUENCE IDEN	rification number: 81:					
	(i) SEQUENCE CHARACTERISTICS:								
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	20 nucleic acid single linear					
	(ix)	FE	ATURE:						
posi	tion	(D) 9 i	OTHER INFORMATION: s A or G; N at position	N at position 16 is C or T; N at ons 3, 6 and 17 is A, T, G or C.	:				
	(xi)	SEQ	UENCE DESCRIPTION: SE	Q ID NO: 81:					
ACNA	.CNGA1	JA T	ggcagnnga	20					
				. *					
(2)	INFO	TAMS	ION FOR SEQUENCE IDEN	TIFICATION NUMBER: 82:					
	(i) S	EQU	ENCE CHARACTERISTICS:						
	/	(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	20 nucleic acid single linear					
	(½x)	FE.	ATURE:						
posi	/ tion			N at position 3 is C or T; N at ons 9, 15 and 18 is A, T, G or C.					
/	(xi)	SEQ	UENCE DESCRIPTION: SE	Q ID NO: 82:					

GANGCNNTNG CNGCNNTNAA

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:

20 CANCANGTNT GGGCNGCNAA (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 83: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 (B) TYPE: nucleic acid (C) STRANDEDNESS: single linear (D) TOPOLOGY: (ix) FEATURE: (D) OTHER INFORMATION: N at position 3 is Cor T; N at position 15 is A or G; N at positions 9, 15 and 18 is/A, T, G or C; N at position 12 is A, C or T. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83: 20 TTNGTNGTNA TNGANGGNAA (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 84: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 (B) TYPE: nucletic acid sing/le (C) STRANDEDNESS: (D) TOPOLOGY: limear (ix) FEATURE: (D) OTHER INFORMATION: /N at positions 9 and 15 is C or T; N at position 3 is A or G; N at positions 6, 12 and 18 is A, T, G or C. (xi) SEQUENCE DESCRIPTION / SEQ ID NO: 84: AANGGNGANG CNCANACNGA 20 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 85: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURÉ: (D) ϕ THER INFORMATION: N at positions 7 and 15 is C or T; N at position/3 is A or G; N at positions 6, 9, 11, 14 and 17 is A, T, G or C/ (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

20

	(1) 5	EQUE	ENCE CHARACTERISTICS:		
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	20 nucleic acid single linear	/
	(ix)	FE?	ATURE:		
	tions , G c	15	and 18 is A or G; N	N at position 19 is C o at positions 3, 6, 9 and	or T/; N at 1 /2 is
	(xi)	SEQU	JENCE DESCRIPTION: SE	Q ID NO: 86:	
GTNG	GNTCN	IG TI	NCANGANNT		20
(2)	INFOR	MAT	ION FOR SEQUENCE IDEN	TIFICATION NUMBER: 87	' :
	(i) S	EQUI	ENCE CHARACTERISTICS:		
		(B)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	nucleic acid single linear	
	(ix)	FE?	ATURE:		
	posi , G c		ns 15 and 18 is A or	N at positions 9 and 19 G: N at positions 3, 6 a	e is C or T; and 12 is
	(xi)	SEQU	JENCE DESCRIPTION: SE	Q ID NO: 87:	
GTNG	GNAGN	IG Tì	NCANGANNT		20
(2)	INFOR	TAM	ION FOR SEQUENCE IDEN	TIFICATION NUMBER: 88	3:
	(i) S	EQUI	ENCE CHARACTERISTICS:		
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	21 nucleic acid single linear	
	(ix)	FEA	ATURE,		
or T	C; N a	(D) it po or C		N at positions 4, 7 and N at positions 1, 10 ar A, G or T.	
	(xi)	SEØ	, JENCE DESCRIPTION: SE	Q ID NO: 88:	
NACN	TTNTT	ia ki	NNATNTGNC C		21
(2)	INFOF	MAT:	ION FOR SEQUENCE IDEN	TIFICATION NUMBER: 89):
	$(\frac{1}{4})$ s	EQUI	ENCE CHARACTERISTICS:		
/		(B)	LENGTH: TYPE: STRANDEDNESS:	417 nucleic acid single	

	(ix	(D) FE) TOI ATURI		GY:			1:	inea	r							/
and	135	(D) is u	_		INF	ORMA'	rion	: Xa	aa i	n pos	sitio	ons :	14,	23, 9	90, 1	00, 12	6 ,
	(xi)) SE(QUEN	CE D	ESCR:	IPTI	ON:	SEQ :	ID N	D: 89	9:						
TCT										le I						T ATA n Ile 5	53
														cg¢ Arg		1	.01
														GTG Val		1	.49
														GTG Val		1	.97
														CTA Leu		2	45
														TCT Ser 95		2	93
														TGT Cys		3	41
														GGT Gly		3	89
					ATA Ile			ATT Ile	T							4	17
(2)	INFO	ORMAT	rion	FOR	SEOU	, JENCI	IDI	ENTI	FICA	rion	NUME	BER:	9	90:			
					RACT												
		(B) (C)	LEN TYI STI	PÉ: KANDI	EDNES	SS:		s	-		cid						
	(ix)	FEA	AZURI	፭:													
in p	osit	(D) ign	22 d	THER can l	INFO	or (CION 3; N	: N in p	in posi	posit	28 c	16 c can h	can l oe C	oe A or 1	or G [.	; N	
	(xi)	SEÇ	QUENC	CE DI	ESCRI	PTIC	ON: S	SEQ I	D NO	D: 90	:						
CCGI	ATT	CTG (CAGG	ANACI	JC A1	1CCU	SANCO	C UGO	3						3	3	
(2)	VNEC	ימשסר	rton	FOD	e E∩i	TENICE	יחד ק	דירואים	? ፐ ፖ አ ፣	rton	MTIME	DED.		o1.			

	(i) S	SEQUENCE CHARACTERISTICS:		
-		(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	37 nucleic acid single linear	
	(ix)	FEATURE:		
posi	tion.	(D) OTHER INFORMATION: 26 can be A, G or T.	N in position 17 can be A o	r &; N in
	(xi)	SEQUENCE DESCRIPTION: SH	EQ ID NO: 91:	
AAGG	SATCCI	rg cagugtntau gcuccnatua	CCATUGG	37
(2)	INFO	RMATION FOR SEQUENCE IDEN	NTIFICATION NUMBER 92:	
	(i) S	SEQUENCE CHARACTERISTICS	:	
		(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	34 nucleic acid single linear	
	(ix)	FEATURE:		
posi	tion	(D) OTHER INFORMATION: 28 can be A or G; N in p	N in position 19 can be C oposition 31 can be C or T.	r T; N in
	(xi)	SEQUENCE DESCRIPTION: SI	ID NO: 92:	
CCGA	ATTC	rg caggcugant cugguganta	NATG	34
(2)	INFO	RMATION FOR SEQUENCE IDE	NTIFICATION NUMBER: 93:	
	(i) S	SEQUENCE CHARACTERISTICS		
		(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	33 nucleic acid single linear	
	(ix)	FEATURE:		
		(D) OTHER INFORMATION: 22 can be C or T; N in p C or T.	N in position 19 can be C oposition 28 can be A or G; N	r T; N in in position
	(xi)	SEQUENCE DESCRIPTION: SI	EQ ID NO: 93:	
CCGF	ATTC:	rg Caggcugana gngguganta	NAT	33
(2)	INFO	/ RMATION FOR SEQUENCE IDE	NTIFICATION NUMBER: 94:	
	(i) s	SEQUENCE CHARACTERISTICS	:	
ı		(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:	34 nucleic acid single	

	(D) TOPOLOGY:	linear	
(ix)	FEATURE:		
position	(D) OTHER INFORMATION: 22 can be C or T; N in po	N in position 19 can be A osition 32 can be A or G.	or G; N in
(xi)	SEQUENCE DESCRIPTION: SEQ	Q ID NO: 94:	
AGGATCC'	TG CAGUUUCATN TANTCUCCUG	ANTC	34
(2) INFO	RMATION FOR SEQUENCE IDENT	rification number: 95:	
(i) s	SEQUENCE CHARACTERISTICS:		
	(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	34 nucleic acid single linear	
(ix)	FEATURE:		
position position	(D) OTHER INFORMATION: 23 can be C or T; N in po	N in position 20 can be A osition 29 can be A or G;	A or G; N in N in
(xi)	SEQUENCE DESCRIPTION: SE	Q ID NO. 95:	
AAGGATCC'	TG CAGUUUCATN TANTCUCCNC	INTC	34
(2) INFO	RMATION FOR SEQUENCE IDEN	rrication number: 96:	
(i) 8	SEQUENCE CHARACTERISTICS	/	
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	33 nucleic acid single linear	
(ix)	FEATURE:		
position	(D) OTHER INFORMATION: 19 can be A or G.	N in position 16 can be 0	or T; N in
(xi)	SEQUENCE PESCRIPTION: SE	Q ID NO: 96:	
CCGAATTC'	TG CAGCANCANG TUTGGGCUGC	TAA	33
(2) INFO	RMATION FOR SEQUENCE IDEN	TIFICATION NUMBER: 97:	
(i)	/ SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS:	35 nucleic acid single linear	
/	(D) TOPOLOGY:	imear	

				,			
(D) OTHER INFORMATION: N in position 16 can be A or C or T; N in position 19 can be C or T; N in position 22 can be C or T; N in position 28 can be A or G; N in position 34 can be A or G.							
(x	i) SEQ	UENCE DESCRIPTION: SEC	Q ID NO: 97:				
CCGAATTCTG CAGATNTTNT TNATGGANCC UGANG 35							
(2) IN	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 98:						
(i	(i) SEQUENCE CHARACTERISTICS:						
	(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	nucleic acid single linear				
(i:	x) FEA	TURE:					
	(D)	OTHER INFORMATION:	N in position 30 can b	e C or T.			
(x	i) SEQ	UENCE DESCRIPTION: SEG	Q ID NO: 98/:				
CCGAAT	TCTG C	AGGGGGUCC UCCUGCUTTN (CCUGT	35			
(2) IN	(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 99:						
(i	(i) SEQUENCE CHARACTERISTICS:						
	(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	33/ nucleic acid single linear				
(i:	x) FEA	TURE:					
(D) OTHER INFORMATION: N in position 19 can be C or T; N in position 28 can be A or C or T; N in position 31 can be A or G.							
(x	i) SEQ	UENCE DESCRIPTION: SEG	Q ID NO: 99:				
CCGAATTCTG CAGTGGTTNG TUCTUATNGA NGG 33							
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 100:							
(i) SEQU	ENCE CHARACTERISTICS:					
	(B) (C)	LENGTH: TYPE: STEANDEDNESS: TOPOLOGY:	34 nucleic acid single linear				
(i	x) FEA	YURE:					
(D) OTHER INFORMATION: N at position 17, 20, and 26 is Inosinc. Y can be cytidine or thymidine.							
(x	i)/SEQ	UENCE DESCRIPTION: SEG	Q ID NO: 100:				
AAGGATCCTG CAGYTTNGC NGCCCANACY TGRTG 34							

(2)	TNEOI	MATTON FOR SPONDINGE	IDENTIFICATION MIMBER: 10	1.			
(2)	2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 101:						
	(1) 5	SEQUENCE CHARACTERIST					
		(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	33 nucleic acid single linear				
	(ix)	FEATURE:					
		(D) OTHER INFORMATION 22 can be C or T; N is A or G.	ON: N in position 16 can be in position 28 can be A or G	C or T; N in			
	(xi)	SEQUENCE DESCRIPTION	: SEQ ID NO: 101:				
AAGO	GATCC	G CAGGCNTCUG GNTCCAT	AAN AAN	33			
(2)	INFO	RMATION FOR SEQUENCE	IDENTIFICATION NUMBER: 10	2:			
	(i) s	SEQUENCE CHARACTERIST	rcs:				
		(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	33 nucleic acid single linear				
	(ix)	FEATURE:					
		(D) OTHER INFORMATIO	ON:/N in position 19 can be	A or G.			
	(xi)	SEQUENCE DESCRIPTION	:/SEQ ID NO: 102:				
AAG	BATCC:	rg cagacuggna augcuget	JGG UCC	33			
(2)	INFO	RMATION FOR SEQUENCE	IDENTIFICATION NUMBER: 10	13:			
	(i) S	SEQUENCE CHARACTERIST	ICS:				
		(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	35 nucleic acid single linear				
	(ix)	FEATURE:					
pos:	ition ition	(D) OTHER INFORMATION 20 can be C or T; N : 32 can be A or G.	ON: N in position 14 can be in position 23 can be A or G	C or T; N in ; or T; N in			
	(xi)	SEQUENCE DESCRIPTION	: SEQ ID NO: 103:				
AAG	GATCC'	rg cagnttuccn tcnatua	CUA CNAAC	35			
(2)	INFO	RMATION FOR SEQUENCE :	IDENTIFICATION NUMBER: 10	04:			
	(i) SEQUENCE CHARACTERISTICS:						
		(A) LENGTH: (B) TYPE: (C) STRANDEDNESS:	33 nucleic acid single				

linear (D) TOPOLOGY: (ix) FEATURE: (D) OTHER INFORMATION: N in position 4 can be A or G; N in position 7 cna be C or T; N in position 10 can be A or G; N in position 13 can be C or T. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104: CATNTANTCN TANTCTCUGC AAGGATCCTG CAG 33 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 105: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: nucleic ac/d (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N in position 16 can be A or G; N in position 22 can be C or T; N in position 28 can be C or T. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105: CCGAATTCTG CAGAANGGUG ANGCUCANAC UGA 33 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 106: (i) SEQUENCE CHARACTERISTACS: (A) LENGTH: (B) TYPE: nucleic acid (C) STRANDEDNESS single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER LAFORMATION: N in position 6 can be C or T; N in position 12 can be C/or T; N in position 15 can be C or T. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106: GCUGCNAAUG CNTCNTTUGC AAGGATCCTG CAG 33 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 107: (i) SEQUÉNCE CHARACTERISTICS: (A) LENGTH: 33 ∥B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N in position 12 can be C or T; N in position 15 can be C or T. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	108:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	30 nucleic acid single linear	
	(ix) FEATURE:		
posi	(D) OTHER INFORMATION: ition 9 can be A or G.	N in position 6 can	be A or G; N in
	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 108:	
TCUC	GCNAANT AUCCUGCAAG GATCCTGCAG		30
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	109:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	38 nucleic acid single linear	
•	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 109:	
CATO	CGATCTG CAGGCTGATT/CTGGAGAATA	TATGTGCA	38
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	110:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	37 nucleic acid single linear	
	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 110:	
AAGO	GATOCTG CAGCCACATC TCGAGTCGAC	ATCGATT	37
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	111:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	37 nucleic acid single linear	
	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 111:	

CCG	ATTCI	rg cz	AGTGATCAG CAAACTAGGA	AATGACA		37/
(2)	INFO	RMAT	ION FOR SEQUENCE IDEN	TIFICATION NUMBER:	112:	/
	(i) S	SEQU!	ENCE CHARACTERISTICS:			
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	37 nucleic acid single linear		
	(xi)	SEQ	UENCE DESCRIPTION: SE	Q ID NO: 112:		
CATO	CGATC	rg c	AGCCTAGTT TGCTGATCAC	TTTGCAC		37
(2)	INFO	RMAT	ION FOR SEQUENCE IDEN	TIFICATION NUMBER:	113:	
	(i) S	SEQU:	ENCE CHARACTERISTICS:			
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	3/7 nucleic acid single linear		
	(xi)	SEQ	UENCE DESCRIPTION: SE	Q ID NO: 113:		
AAG	GATCC:	rg C	AGTATATTC TCCAGAATCA	GCCAGTG		37
(0)	TMEG	- M - M - M - M - M - M - M - M - M - M	ION FOR SEQUENCE IDEN	MIRION NUMBER .	114.	
(2)				IIFICATION NUMBER:	114:	
	(1) :		ENCE CHARACTERISTICS:			
			STRANDEDNESS:	34 nucleic acid single linear		
	(xi)	SEQ	UENCE DESCRIPTION: SE	Q ID NO: 114:		
AAG	GATCC'	rg c	AGGCACGCA GTAGGCATCT	CTTA		34
(2)	INFO	гиат	ION FOR SEQUENCE IDEN	TIFICATION NUMBER:	115:	
	(i)/s	/ SEQU	ENCE CHARACTERISTICS:			
/		(B)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	35 nucleic acid single linear		
	(xi)	SEQ	UENCE DESCRIPTION: SE	Q ID NO: 115:		
CCG	AATTC'	TG C	AGCAGAACT TCGCATTAGC	AAAGC		35
(2)	INFO	RMAT	ION FOR SEQUENCE IDEN	TIFICATION NUMBER:	116:	
	(1)	SEOII	ENCE CHARACTERISTICS.			

				,
		33 nucleic acid single linear		
	(xi) SEQUENCE DESCRIPTION: SE	EQ ID NO: 116:		
	CATCCCGGGA TGAAGAGTCA GGAGTCTGTG	GCA /	/	33
	(2) INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	117:	
	(i) SEQUENCE CHARACTERISTICS:	:		
	(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	39 nucleic acid single linear		
	(xi) SEQUENCE DESCRIPTION: SE	EQ ID NØ: 117:		
	ATACCCGGGC TGCAGACAAT GAGATTTCAC	ACACCTGCG		39
	(2) INFORMATION FOR SEQUENCE IDEN	NT/FICATION NUMBER:	118:	
	(i) SEQUENCE CHARACTERISTICS	/ :		
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	36 nucleic acid single linear		
	(xi) SEQUENCE DESCRIPTION: SE	EQ ID NO: 118:		
	AAGGATCCTG CAGTTTGGAA CCTGCCACAG	ACTCCT		36
	(2) INFORMATION FOR SEQUENCE IDEN	NTIFICATION NUMBER:	119:	
	(i) SEQUENCE CHARACTERISTICS	:		
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	39 nucleic acid single linear		
	(xi) SEQUENCE DESCRIPTION: SE	EQ ID NO: 119:		
	ATACCCGGGC TGCAGATGAG ATTTCACACA	CCTGCGTGA		39
	(2) INFORMATION FOR SEQUENCE IDEN	NTIFICATION NUMBER:	120:	
	(i) SEQUENCE CHARACTERISTICS	:		
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	12 amino acid linear		
/	(vi) SPOHENCE DESCRIPTION: SI			

His 1	Gln Val Trp Ala Ala Lys Ala Al 5	a Gly Leu Lys 10
(2)	INFORMATION FOR SEQUENCE IDENT	IFICATION NUMBER: 121:
	(i) SEQUENCE CHARACTERISTICS:	
	(B) TYPE: (C) STRANDEDNESS:	16 amino acid linear
	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO: 121:
Gly 1	Gly Leu Lys Lys Asp Ser Leu Le 5	u Thr Val Arg Leu Gly Ala Asn 10 15
(2)	INFORMATION FOR SEQUENCE IDENT	IFICATION NUMBER: 122:
	(i) SEQUENCE CHARACTERISTICS:	
	(C) STRANDEDNESS:	73 amino acid linear
	(ix) FEATURE:	
	(D) OTHER INFORMATION:	Xaa in position 12 is unknown.
	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO: 122:
Leu 1	Gly Ala Trp Gly Pro Pro Ala Ph	e Pro Val Xaa Tyr 10
(2)	INFORMATION FOR SEQUENCE IDENT	IFICATION NUMBER: 123:
	(i) SEQUENCE CHARACTERISTICS:	
	(B) TYPE: (C) STRANDEDNESS:	23 amino acid linear
	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO: 123:
Leu 1	Leu Thr Val Arg Leu Gly Ala Tr	p Gly His Pro Ala Phe Pro Ser 10 15
Cys	Gly Arg Leu Lys Glu Asp 20	
(2)	/INFORMATION FOR SEQUENCE IDENT	IFICATION NUMBER: 124:
	(i) SEQUENCE CHARACTERISTICS:	
/	(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:	13 amino acid

		(D) TOP	OLOGY:		linear	
	(ix) H	FEATURE	S :			/
	,	(D) OI	THER INFO	RMATION:	Xaa in position 10 is unk	nown.
	(xi) S	SEQUENC	CE DESCRI	PTION: SE	Q ID NO: 124:	
Tyr 1	Ile Ph	ne Phe	Met Glu 5	Pro Glu A	la Xaa Ser Ser Gly 10	
(2)	INFORM	MOITAM	FOR SEQU	JENCE IDEN	TIFICATION NUMBER: / 125:	
	(i) SI	EQUENCE	E CHARACT	TERISTICS:		
				SS:	23 amino acid linear	
	(xi) S	SEQUENC	CE DESCRI	PTION: SE	Q ID NO: 125:	
Lys 1	Glu As	sp Ser	Arg Tyr 5	Ile Phe P	he Met Glu Pro Glu Ala Asn 10 15	Ser
Ser	Gly G	ly Pro 20	Gly Arg	Leu		
(2)	INFORM	MATION	FOR SEQU	JENCE IDEN	rification number: 126:	
	(i) SI	EQUENCE	E CHARACI	TERISTICS:		
				SS:	14 amino acid linear	
	(xi) s	SEQUENC	CE DESCRI	IPTION: SE	Q ID NO: 126:	
Val 1	Ala G	ly Ser	Lys Lew	Val Leu A	rg Cys Glu Thr Ser Ser 10	
(2)	INFOR	MATION	FOR SEQU	JENCE IDEN	TIFICATION NUMBER: 127:	
	(i) S	EQUENCI	E CHARACT	TERISTICS:		
				SS:	16 amino acid linear	
	(xi) :	SEQUEN	CE DESCRI	IPTION: SE	Q ID NO: 127:	
Glu 1	Tyr/Ly	ys Cys	Leu Lys 5	Phe Lys T	rp Phe Lys Lys Ala Thr Val 10 15	
(2)	INFORI	MATION	FOR SEQU	JENCE IDEN	TIFICATION NUMBER: 128:	
	(i) S	EQUENCI	E CHARACT	TERISTICS:		

		/
	(A) LENGTH: 26 (B) TYPE: amin (C) STRANDEDNESS:	o acid
	(D) TOPOLOGY: line	ar /
	(xi) SEQUENCE DESCRIPTION: SEQ ID	NO: 128:
Cys 1	s Glu Thr Ser Ser Glu Tyr Ser Ser Le 1 5 1	u Lys Phe Lys Trp Phe Lys 0 15
Asn	n Gly Ser Glu Leu Ser Arg Lys Asn Ly 20 25	s
(2)) INFORMATION FOR SEQUENCE IDENTIFIC	ATION NUMBER: 129:
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 13 (B) TYPE: amir (C) STRANDEDNESS: (D) TOPOLOGY: line	o acid
	(ix) FEATURE:	/
	(D) OTHER INFORMATION: Xaa	in position 12 is unknown.
	(xi) SEQUENCE DESCRIPTION: SEQ TD	NO: 129:
Lys 1	s Ala Ser Leu Ala Asp Ser Gly Glu Ty 1 5	r Met Xaa Lys O
(2)) INFORMATION FOR SEQUENCE IDENTIFIC	CATION NUMBER: 130:
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 23 (B) TYPE: amin (C) STRANDEDNESS: (D) TOPOLOGY: line	o acid ear
	(xi) SEQUENCE DESCRIPTION: SEQ ID	NO: 130:
Glu 1	u Leu Arg Ile Ser Lys Ala Ser Leu Al 1 5	a Asp Ser Gly Glu Tyr Met .0 15
Cys	s Lys Val Ile Ser Lys Leu 20	
(2)) INFORMATION FOR SEQUENCE IDENTIFIC	CATION NUMBER: 131:
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 12	
	(B) TYPE: amin (C) STRANDEDNESS: (D) TOPOLOGY: line	no acid ear
	(xi) SEQUENCE DESCRIPTION: SEQ ID	NO: 131:
Ala 1	a Ser Leu Ala Asp Glu Tyr Glu Tyr Mo 1 5	et Arg Lys 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION	NUMBER: 132:
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 22	
(B) TYPE: amino acid (C) STRANDEDNESS:	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13	
Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser 1 5 10	Gly G1u Tyr Met Cys 15
Lys Val Ile Ser Lys Leu 20	
(2) INFORMATION FOR SEQUENCE IDENTIFICATION	NUMBER: 133:
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 744	
(B) TYPE: nucleic ac (C) STRANDEDNESS: single	10
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ/ID NO: 13	
CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG His Gln Val Trp Ala Ala Lys Ala Gly	GGC TTG AAG AAG GAC TCG CTG 55 Gly Leu Lys Lys Asp Ser Leu 10 15
1 5	
CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro 20 25	GCC TTC CCC TCC TGC 103 Ala Phe Pro Ser Cys 30
GGG CGC CTC AAG GAG GAC AGG TAC ATC TTC	TTC ATG GAG CCC GAG 151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe 35 40	Phe Met Glu Pro Glu 45
GCC AAC AGC AGC GGC GGC CCC GGC CTT CCG Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro	
	60
TCT CGA GAC GGG CCG/GAA CCT CAA GAA GGA GGT Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly	
65 70 75 75	80
CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu	
85 90	95
TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys	
100 105	110
TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn	
115 120	125
CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln	
130 135	140
/	•

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr 155 150 ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn 170 165 ATC ACC ATT GTG GAG TCA AAC GGT AAG AGA TGC CTA CTG/CGT GCT ATT Ile Thr Ile Val Glu Ser Asn Gly Lys Arg Cys Leu Leú Arg Ala Ile 190 185 TCT CAG TCT CTA AGA GGA GTG ATC AAG GTA TGT GGT/CAC ACT 625 Ser Gln Ser Leu Arg Gly Val Ile Lys Val Cys Gly His Thr 200 TGAATCACGC AGGTGTGTGA AATCTCATTG TCAACAAATA AAAATCATGA AAGGAAAAAA 685 AAAAAAAAA AATCGATGTC GACTCGAGAT GTGGCTGCAG GTCGACTCTA GAGGATCCC 744 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: (i) SEQUENCE CHARACTERISTICS: 11**9**3 (A) LENGTH: núcleic acid (B) TYPE: (C) STRANDEDNESS: #ingle (D) TOPOLOGY: /linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134: CCTGCAG CAT CAA GTG TGG GCG GQG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG 55 His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TGC 103 Leu Thr Val Arg Leu Gly A/a Trp Gly His Pro Ala Phe Pro Ser Cys 25 20 GGG CGC CTC AAG GAG GAC/AGC AGG TAC ATC TTC ATG GAG CCC GAG 151 Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu 40 GCC AAC AGC AGC GGC GGG CCC GGC CTT CCG AGC CTC CTT CCC CCC 199 Ala Lys Ser Ser Cly/Cly Pro Cly Arg Leu Pro Ser Leu Leu Pro Pro TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG 247 Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gln Pro Gly Ala Val CAA CGG TGC GOC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG 295 Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu 85 TCT GTG GCA/GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA 343 Ser Val Alá Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu 100 105 TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC 391 Tyr Ser/Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser 120

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG 439 Arg Lys Asn Lys Gly Gly Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys 130 135 TCA GGA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT 487 Ser Gly Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr 150 ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC 535 Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Sér Ala Asn 165 ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT AÇÁ GCT GGG ACA 583 Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr 190 180 185 AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA AÇT TTC TGT GTG AAT 631 Ser His Leu Val Lys Ser Ala Glu Lys Glu Lys Thr Phe Cys Val Asn 200 205 195 GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 679 Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr 210 215 220 TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 727 Leu Cys Lys Cys Gln Pro Gly Phe Thr Gl/y Ala Arg Cys Thr Glu Asn 235 225 GTG CCC ATG AAA GTC CAA ACC CAA GAA/AGT GCC CAA ATG AGT TTA CTG 775 Val Pro Met Lys Val Gln Thr Gln Gly Ser Ala Gln Met Ser Leu Leu 250 GTG ATC GCT GCC AAA ACT ACG TAATGGCCAG CTTCTACAGT ACGTCCACTC 826 Val Ile Ala Ala Lys Thr Thr CCTTTCTGTC TCTGCCTGAA TAGCGQATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC 886 TCCCCTCAGA TTCCTCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCTCT 946 GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT 1006 GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT 1066

ACTGTGATAC GACATGATAC TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA 1126 GTCAAAAAAA AAAAAAAAAA AAAAAATCGA TGTCGACTCG AGATGTGGCT GCAGGTCGAC 1186

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 135

- (i) SEQUENCE CHARACTERISTICS:
 - (A)/ LENGTH: 1108 base pairs
 - (B/) TYPE: nucleic acid
 - (¢) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

TCTAGAG

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 8...778
- (D) OTHER INFORMATION:

1193

(2	ki) S	EQUE	ENCE	DESC	CRIPT	CION:	SEC) ID	NO:	135:				/	
CCTGCAG	CAT His 1	CAA Gln	GTG Val	TGG Trp	GCG Ala 5	GCG Ala	AAA Lys	GCC Ala	GGG Gly	GGC Gly 10	TTG Leu	AAG Lys	AAG Lys	GAC Asp	49
TCG CTG Ser Leu 15	CTC Leu	ACC Thr	GTG Val	CGC Arg 20	CTG Leu	GGC Gly	GCC Ala	TGG Trp	GGC Gly 25	CAC His	CCC Pro	GCC/ Al/a	TTC Phe	CCC Pro 30	97
TCC TGC Ser Cys	GGG Gly	CGC Arg	CTC Leu 35	AAG Lys	GAG Glu	GAC Asp	AGC Ser	AGG Arg 40	TAC Tyr	ATC Ile	TTC/ Phe	TTC Phe	ATG Met 45	GAG Glu	145
CCC GAG Pro Glu	GCC Ala	AAC Asn 50	AGC Ser	AGC Ser	GGC Gly	GGG Gly	CCC Pro 55	GGC Gly	CGC Arg	CTT Len	CCG Pro	AGC Ser 60	CTC Leu	CTT Leu	193
CCC CCC Pro Pro	TCT Ser 65	CGA Arg	GAC Asp	GGG Gly	CCG Pro	GAA Glu 70	CCT Pro	CAA Gln	GAA Glu	GGA Gly	GGT Gly 75	CAG Gln	CCG Pro	GGT Gly	241
GCT GTG Ala Val 80															289
CAG GAG Gln Glu 95															337
TCT GAA Ser Glu	TAC Tyr	TCC Ser	TCT Ser 115	CTC Leu	AAG Lys	TTC Phe	AAG Lys	TGG Trp 120	TTC Phe	AAG Lys	AAT Asn	GGG Gly	AGT Ser 125	GAA Glu	385
TTA AGC Leu Ser															433
GGG AAG Gly Lys	TCA Ser 145	GAA Glu	CTT Leu	CGC Arg	ATT Ile	AGC Ser 150	AAA Lys	GCG Ala	TCA Ser	CTG Leu	GCT Ala 155	GAT Asp	TCT Ser	GGA Gly	481
GAA TAT Glu Tyr 160	Met	Cys		V,a1		Ser	Lys	Leu	Gly	Asn	Asp				529
GCC AAC Ala Asn 175															577
GGG ACA Gly Thr															625
GTG AAT Val Asn															673
AGA TAC Arg Tyr															721
AAC TAC Asn Tyr															769

CTG CCT GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC TCCCCTCAG 827 Leu Pro Glu

ATTCCGCCTA GAGCTAGATG CGTTTTACCA GGTCTAACAT TGACTGCCTC TGCCTGTCGC ATGAGAACAT TAACACAAGC GATTGTATGA CTTCCTCTGT CCGTGACTAG TÆGGCTCTGA GCTACTCGTA GGTGCGTAAG GCTCCAGTGT TTCTGAAATT GATCTTGAAT /TACTGTGATA 1007 CGACATGATA GTCCCTCTCA CCCAGTGCAA TGACAATAAA GGCCTTGAAX AGTCAAAAAA 1067 AAAAAAAAA AAAAAATCGA TGTCGACTCG AGATGTGGCT G

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 136:

245

- (i) SEOUENCE CHARACTERISTICS:
 - (A) LENGTH:

(B) TYPE:

nucleic acid

(C) STRANDEDNESS: (D) TOPOLOGY:

single linear

- (ix) FEATURE:
 - OTHER INFORMATION: N in position 214 is unknown.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

AGTTTCCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC 60 GGCGGCTGCC CAGGCGATGC GAGCGCGGGC/CGGACGGTAA TCGCCTCTCC CTCCTCGGGC 120 TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC 180 CCAGCGGCGC GCCAGCAGGA GCCACCCÓGC GAGNCGTGCG ACCGGGACGG AGCGCCCGCC 240 AGTCCCAGGT GGCCCGGACC GCACG/TTGCG TCCCCGCGCT CCCCGCCGGC GACAGGAGAC 300 GCTCCCCCC ACGCCGCGC CGCCTCGGCC CGGTCGCTGG CCCGCCTCCA CTCCGGGGAC 360 AAACTTTTCC CGAAGCCGAT CÉCAGCCCTC GGACCCAAAC TTGTCGCGCG TCGCCTTCGC 420 CGGGAGCCGT CCGCGCAGAG/CGTGCACTTC TCGGGCGAG ATG TCG GAG CGC AGA 474 Met Ser Glu Arg Arg

GAA GGC AAA GGC AXG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG 522 Glu Gly Lys Gly Lys Gly Lys Gly Lys Lys Asp Arg Gly Ser Gly

AAG AAG CCC GTØ CCC GCG GCT GGC GGC CCG AGC CCA G 559 Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala /25 3.0

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 137:
 - SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:

252

(B) TYPE:

nucleic acid

(C) STRANDEDNESS:

single

(D) TOPOLOGY:

linear

A or	G.	(D)	ro	HER	INFO	RMAT	CION:	N	in p	osit	ion	8 cc	ould	be e	ithe	r
	(xi)	SEÇ	QUENC	CE DE	SCRI	PTIC	on: S	SEQ]	D NO): 13	17:		/			
CC (CAT (His (CAN C	GTG 7	GG G	CG (Ala A	ECG A	AAA C	GCC (GG (GC T Gly I 10	TTG A	AAG A	AAG (SAC S	CCG Ser 15	47
CTG Leu	CTC Leu	ACC Thr	GTG Val	CGC Arg 20	CTG Leu	GGC Gly	GCC Ala	TGG Trp	GGC Gly 25	CAC His	CCC Pro	GCC Ala	TTC Phe	CCC Pro 30	TCC Ser	95
TGC Cys	GGG Gly	CGC Arg	CTC Leu 35	AAG Lys	GAG Glu	GAC Asp	AGC Ser	AGG Arg 40	TAC Tyr	ATC Ile	TTC Phe	TTC Phe	ATG Met 45	GAG Glu	CCC Pro	143
GAG Glu	GCC Ala	AAC Asn 50	AGC Ser	AGC Ser	GGC Gly	GGG Gly	CCC Pro 55	GGC Gly	CGC Arg	CTT Leu	CCG Pro	AGC Ser 60	CTC Leu	CTT Leu	CCC Pro	191
CCC Pro	TCT Ser 65	CGA Arg	GAC Asp	GGG Gly	CCG Pro	GAA Glu 70	CCT Pro	CAA Gln/	GAA Glu	GGA Gly	GGT Gly 75	CAG Gln	CCG Pro	GGT Gly	GCT Ala	239
		CGG Arg	TGC Cys	G				/								252
(2)	INFO	ORMAC	rion	FOR	SEQU	JENG	/ E IDE	ENTI	FICA	rion	NUMI	BER:	:	138:		
(2)						JENO TERIS			FICA	rion	NUMI	BER:		138:		
(2)		SEQUAL (A)		E CHA NGTH: PE: RANDE	ARACT	reris		5: 1' ni s:	78_	ic ad		BER:		138:		
(2)	(i)	SEQU (A) (B) (C) (D)	JENCI LEN TYI STI	E CHA NGTH: PE: RANDE	ARACT EDNES	reris	STICS	5: 1' n: s: 1:	78 ucle: ingle inear	ic ad e r	cid	BER:		138:		
CCT	(i) (xi)	SEQUAL (A) (B) (C) (D) SEQUAL (C)	JENCE LEN TYI TOI QUENC CCC Arg	E CHANGTH: PE: RANDE POLOG CE DE	ARACT EDMES ESCRI	TERIS	ON: S AGA His	S: 1' nu s: 1: EEQ : TGA Lys	78 ucle: ingle inea: ID NO AGA Ser	ic ace e r D: 13	eid 38: AGG Glu	AGT Ser	CTG	TGG Ala	Gly	48
CCT Leu 1 GTT	(i) (xi) TGC Pro	SEQUENT (A) (B) (C) (D) SEQUENT (C) Pro	JENCE LEN TYI STI TOI QUENC	GCT Leu	ARACT EDMES ESCRI TGA Lys	TERIS	ON: S AGA His GCG	I' nv s: l: SEQ I TGA Lys	78 ucle: ingle inea: ID NO AGA Ser 10 CCA	ic ace e r O: 13 GTC Gln GTT	eid 38: AGG Glu CTG	AGT Ser	CTG Val	TGG Ala 15 CCT	Gly	48 96
CCT Leu 1 GTT Ser	(i) (xi) TGC Pro CCA Lys	SEQUENCE (A) (B) (C) (D) SEQUENCE CTC Pro AAC Leu TCA	JENCE LEN STE TOE CCC Arg TAG Val 20	GCT Leu GGT GGT GGT GGT	ARACT EDMES ESCRI TGA Lys TTC Arg	FERIS SS: IPTIC AAG Glu GGT	ON: S AGA His GCG Glu	S: 1' s: 1: SEQ I TGA Lys AGA Thr 25 GGA	78 ucle: ingle inea: ID NO AGA Ser 10 CCA Ser GTG	ic acer cr C: 13 GTC Gln GTT Ser	eid 88: AGG Glu CTG Glu	AGT Ser AAT Tyr	CTG Val ACT Ser 30 GAA	TGG Ala 15 CCT Ser	CTC Leu ACA	
CCT Leu 1 GTT Ser TCA Lys	(i) (xi) TGC Pro CCA Lys AGT Phe	SEQUENCE (A) (B) (C) (D) SEQUENCE (CTC Pro	JENCE LEN TYPE STE TOPE CCC Arg TAG Val 20 AGT Trp	GCT Leu GGT Phe TCA	TCA Lys	SS: IPTIC AAG Glu GGT Cys	ON: SAGA His GCG Glu ATG Gly 40	S: 1' SEQ : TGA Lys AGA Thr 25 GGA Ser	78 acle: ingle inear ID NO AGA Ser 10 CCA Ser GTG Glu GGC	ic ace r D: 13 GTC Gln GTT Ser AAT Leu	eid 88: AGG Glu CTG Glu TAA Ser	AGT Ser AAT Tyr GCC Arg	CTG Val ACT Ser 30 GAA	TGG Ala 15 CCT Ser	CTC Leu ACA	96
CCT Leu 1 GTT Ser TCA Lys	(i) (xi) TGC Pro CCA Lys AGT Phe CAO Gly 50	SEQUENCE (A) (B) (C) (D) SEQUENCE (CTC Pro	JENCE LEN TYPE STE TOD CCC Arg TAG Val 20 AGT Trp	GCT Leu GGT Phe TCA Lys	TGA Lys TCA Lys AGA	GGT Cys AGA Asn TAC Gln	ON: SAGA His GCG Glu ATG Gly 40 AGA Lys	TGA Lys AGA Thr 25 GGA Ser AAA	78 aclesingle ineas ID NO AGA Ser 10 CCA Ser GTG Glu GGC Pro	ic ace r D: 13 GTC Gln GTT Ser AAT Leu CGG Gly	aid 38: AGG Glu CTG Glu TAA Ser	AGT Ser AAT Tyr GCC Arg 45	CTG Val ACT Ser 30 GAA Lys	TGG Ala 15 CCT Ser	CTC Leu ACA	96 144

(ix) FEATURE:

(B) TYPE:	.22 nucleic acid ningle ninear
(') CHONINGE DECORADED CON	TD NO. 130.
(xi) SEQUENCE DESCRIPTION: SEQ G AAG TCA GAA CTT CGC ATT AGC AAA G	
Lys Ser Glu Leu Arg Ile Ser Lys A	Ala Ser Leu Ala Asp Ser Gly 10 15
GAA TAT ATG TGC AAA GTG ATC AGC AAA Glu Tyr Met Cys Lys Val Ile Ser Lys 20	A CTA GGA AAT GAC AGT GCC TCT 94 E Leu Gly Asn Asp Ser Ala Ser 25 30
GCC AAC ATC ACC ATT GTG GAG TCA AAC Ala Asn Ile Thr Ile Val Glu Ser Asn 35	
(2) INFORMATION FOR SEQUENCE IDENTI	FICATION NUMBER: 140:
(i) SEQUENCE CHARACTERISTICS:	
(B) TYPE: n (C) STRANDEDNESS: 5	aucleic acid ringle ringar
(xi) SEQUENCE DESCRIPTION: SEQ	ID NO: 140:
TCTAAAACTA CAGAGACTGT ATTTTCATGA TC	CATCATAGT TCTGTGAAAT ATACTTAAAC 60
CGCTTTGGTC CTGATCTTGT AGG AAG TCA G Lys Ser G	GAA CTT CGC ATT AGC AAA GCG 110 Glu Leu Arg Ile Ser Lys Ala 5
TCA CTG GCT GAT TCT GGA GAA TAT ATG Ser Leu Ala Asp Ser Gly Glu Tyr Met 10	
GGA AAT GAC AGT GCC TCT GCC AAC ATC Gly Asn Asp Ser Ala Ser Ala Asn Ile	
AAG AGA TGC CTA CTG CGT GCT ATT TCT Lys Arg Cys Leu Arg Ala Ile Ser 45 50	Gln Ser Leu Arg Gly Val Ile
AAG GTA TGT/GGT CAC ACT TGAATCACGC Lys Val Cys Gly His Thr	AGGTGTGTGA AATCTCATTG 302
TGAACAAATA AAAATCATGA AAGGAAAACT CT	CATGTTTGA AATATCTTAT GGGTCCTCCT 362
GTAAAGCTCT TCACTCCATA AGGTGAAATA GA	ACCTGAAAT ATATATAGAT TATTT 417
(2) INFORMATION FOR SEQUENCE IDENTI	FICATION NUMBER: 141:

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 102 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:	
AG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser 1 5 10 15	47
TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr 20 25 30	95
TCT TCA T Ser Ser Ser 35	102
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 142:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: 69 nucleic acid single linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:	
AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT GTG CCC Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro 1 5 10 15	48
ATG AAA GTC CAA ACC CAA GAA Met Lys Val Gln Thr Gln Glu 20	69
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 143:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 60 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:	
AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met 10 15	48
CCC AGC TTC TAC Ala Ser Phe Tyr	60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 144:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 36 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:	
AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAG Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu 1 5 10	36
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 145:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 27 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:	
AAG CAT CTT GGG ATT GAA TTT ATG/GAG Lys His Leu Gly Ile Glu Phe Met Glu 1 5	27
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 146:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 569 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:	
AAA GCG GAG GAG OTC TAC CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile 1 5 10 15	48
TGC ATC GCG CTG CTC GTG GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Val Tyr Cys 20 25 30	96
AAA ACC AAG AAA CAA CGG AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln Ser 35 40 45	144
CTT CGC TCT GAA AGA AAC ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC Leu Arg Ser Glu Arg Asn Thr Met Met Asn Val Ala Asn Gly Pro His 50 60	192

CAC His 65	CCC Pro	AAT Asn	CCG Pro	CCC Pro	CCC Pro 70	GAG Glu	AAC Asn	GTG Val	CAG Gln	CTG Leu 75	GTG Val	AAT Asn	CAA Gln	TAC Tyr	GTA Val/ 80	240
TCT Ser	AAA Lys	AAT Asn	GTC Val	ATC Ile 85	TCT Ser	AGC Ser	GAG Glu	CAT His	ATT Ile 90	GTT Val	GAG Glu	AGA Arg	GAG Glu	GCG Ala 95	GÁG Glu	288
AGC Ser	TCT Ser	TTT Phe	TCC Ser 100	ACC Thr	AGT Ser	CAC His	TAC Tyr	ACT Thr 105	TCG Ser	ACA Thr	GCT Ala	CAT His	CAT His/ 110	rcc ser	ACT Thr	336
ACT Thr	GTC Val	ACT Thr 115	CAG Gln	ACT Thr	CCC Pro	AGT Ser	CAC His 120	AGC Ser	TGG Trp	AGC Ser	AAT Asn	GGA Gly 125	CAC His	ACT Thr	GAA Glu	384
AGC Ser	ATC Ile 130	ATT Ile	TCG Ser	GAA Glu	AGC Ser	CAC His 135	TCT Ser	GTC Val	ATC Ile	GTG Val	ATG Met 140	TCA Ser	TCC Ser	GTA Val	GAA Glu	432
AAC Asn 145	AGT Ser	AGG Arg	CAC His	AGC Ser	AGC Ser 150	CCG Pro	ACT Thr	GGG Gly	GGC Gly	CCG Pro 155	AGA Arg	GGA Gly	CGT Arg	CTC Leu	AAT Asn 160	480
GGC Gly	TTG Leu	GGA Gly	GGC Gly	CCT Pro 165	CGT Arg	GAA Glu	TGT Cys	AAC Asn	AGC Set 1/10	TTC Phe	CTC Leu	AGG Arg	CAT His	GCC Ala 175	AGA Arg	528
GAA Glu	ACC Thr	CCT Pro	GAC Asp 180	TCC Ser	TAC Tyr	CGA Arg	GAC Asp	TCT/ Ser 1/85	CCT Pro	CAT His	AGT Ser	G A	AAG			569
(2)		SEQ	JENCI	E CHA	ARAC	/	/	S:		rion	NUMI	BER:		147:		
(2)		SEQUAL (A)		E CHA NGTH PE: RANDI	ARACT	rerz:	/	5: 7: n: s:	30	ic ad		BER:		147:		
(2)	(i)	SEQUAL (A)	JENCI LEI TYI STI	E CHA NGTH PE: RANDI POLOG	ARACT : EDNE: GY:	TERIS	/ STIC	7: n: s: 1:	30 ucle: ingle inea:	ic ad e r	cid	BER:		147:		
G T	(i) (xi)	SEQUAL (A) (B) (C) (D) SEQUAL (A)	JENCI LEI TYI STI TOI QUENC	E CHANGTH PE: RANDI POLOG CE DA	ARACT EDNES GY: ESCRI	TERIS	/ STICS ON: {	7: ni s: 1: SEQ	30 ucle: ingle inea: ID NO CT CO	ic ader r O: 14	cid	CA C	CT G	TA G. al A	AT sp 15	46
G TZ Ty	(i) (xi) AT Gr yr Va 1 CAC	SEQUENCE (A) (B) (C) (D) SEQUENCE (A) SEQUEN	JENCI LEI TYI STI TOI QUENC	E CHANGTH PE: RANDI POLOG CE DI CA AT I a Mo	ARACT EDNES ESCRI TG AG t Tl 5	SS: IPTIC CC AC CCC	ON: S	7: 7: 8: 1: SEQ CG GG TCA	30 ucle: ingle inea: ID No CT Co la A:	ic ace r O: 1. GT A rg Mc 10	cid 47: TG T	CA Coer Po	CT G ro V ATG	TA G. al A	sp 15 CCG	46 94
G TA	(i) (xi) AT GT Yr Va 1 CAC His	SEQUENCE OF SEQUEN	JENCI LEI TYI STI TOI QUENC CA GO Er A	E CHANGTH PE: RANDI POLOG CE DA AGC Ser 20 ACG	ARACT EDINES ESCRI IG AG ET TI TCC Ser ACG	SS: IPTIC CC AC nr Ti CCC Pro	ON: S CC CC hr P: AAG Lys	SEQ TCA Ser ATG	CCC Pro	ic acer r O: 1.4 GT A'rg Mc 10 CCT Pro	cid 47: TG TG et SG	CA Cer Pose	CT G ro V ATG Met GTC	TA G al A TCC Ser 30 AGT	sp 15 CCG Pro	
G TY TTC Phe CCC Pro	(xi) (xi) AT GT Yr Va 1 CAC His GTG Val	SEQUENCE OF SECUENCE OF SECUEN	JENCI LEI TYI STI TOI QUENC CA GC Er A Pro AGC Ser 35	MGTH PE: RANDI POLOG CE DI CA AT AGC Ser 20 ACG Thr	ARACT EDINES ESCRI TG AG TCC Ser ACG Thr	SS: IPTIC CCC AC Pro GTC Val	ON: S CC CC hr P: AAG Lys TCC Ser CTG	SEQ CG GG TCA Ser ATG AtG Met 40 CTC	CCC Pro	ic ace r O: 1.4 GT A' rg Mc 10 CCT Pro TCC Ser	cid 47: TG TG et SG TCG Ser ATG	CA Cer Post GAA Glu GCG Ala	CT G ro V ATG Met GTC Val 45 CCA	TA GA al A TCC Ser 30 AGT Ser	SP 15 CCG Pro CCC Pro	94

,

AAC Asn 80	CCC Pro	GCG Ala	CAT His	GAG Glu	AGC Ser 85	AAC Asn	AGC Ser	CTG Leu	CCC Pro	CCC Pro 90	AGC Ser	CCC Pro	TTG Leu	AGG Arg	ATA Ile /95	286
GTG Val	GAG Glu	GAT Asp	GAG Glu	GAA Glu 100	TAT Tyr	GAA Glu	ACG Thr	ACC Thr	CAG Gln 105	GAG Glu	TAC Tyr	GAA Glu	CCA Pro	GCT Ala 110	CAA Gln	334
GAG Glu	CCG Pro	GTT Val	AAG Lys 115	AAA Lys	CTC Leu	ACC Thr	AAC Asn	AGC Ser 120	AGC Ser	CGG Arg	CGG Arg	GCC Ala	AAA Lys 125	AGA Arg	ACC Thr	382
AAG Lys	CCC Pro	AAT Asn 130	GGT Gly	CAC His	ATT Ile	GCC Ala	CAC His 135	AGG Arg	TTG Leu	GAA Glu	ATG Met	GAC Asp 140	AAC Asn	AAC Asn	ACA Thr	430
GGC Gly	GCT Ala 145	GAC Asp	AGC Ser	AGT Ser	AAC Asn	TCA Ser 150	GAG Glu	AGC Ser	GAA Glu	ACA Thr	GAG Glu 155	GAT Asp	GAA Glu	AGA Arg	GTA Val	478
GGA Gly 160	GAA Glu	GAT Asp	ACG Thr	CCT Pro	TTC Phe 165	CTG Leu	GCC Ala	ATA Ile	CAG Gln	AAC Asn 170	CCC Pro	CTG Leu	GCA Ala	GCC Ala	AGT Ser 175	526
CTC Leu	GAG Glu	GCG Ala	GCC Ala	CCT Pro 180	GCC Ala	TTC Phe	CGC Arg	CTG Leu	GTC Val 185	GAC Asp	AGC Ser	AGG Arg	ACT Thr	AAC Asn 190	CCA Pro	574
ACA Thr	GGC Gly	GGC Gly	TTC Phe 195	TCT Ser	CCG Pro	CAG Gln	GAA Glu	GAA Glu 200	TTG Leu	CAG Gln	GCC Ala	AGG Arg	CTC Leu 205	TCC Ser	GGT Gly	622
GTA Val	ATC Ile	GCT Ala 210	AAC Asn	CAA Gln	GAC Asp	CCT Pro	ATC 1/1e 215	GCT Ala	GTC Val	TAA	AACC	GAA .	ATAC.	ACCC.	AT	672
AGA'	TTCA(CCT (GTAA	AACT'	TT A	TTT	ATAT.	A AT	AAAG'	TATT	CCA	CCTT.	AAA	TTAA	ACAA	730

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: /1652 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA (ix) FEATURE:
- - (A) NAME/KEY: Coding Sequence (B) LOCATION: 459...1181

 - (D) OTHER INFORMATION:
- (xi/ SEQUENCE DESCRIPTION: SEQ ID NO:148:

,						
AGTTTCCCCC	CCCAACTTGT	CGGAACTCTG	GGCTCGCGCG	CAGGGCAGGA	GCGGAGCGGC	60
GGCGGCTGCC	CAGGCGATGC	GAGCGCGGGC	CGGACGGTAA	TCGCCTCTCC	CTCCTCGGGC	120
TGCGAGCGCG	CCGGACCGAG	GCAGCGACAG	GAGCGGACCG	CGGCGGGAAC	CGAGGACTCC	180
CCAGCGGCGC	GCCAGCAGGA	GCCACCCCGC	GAGCGTGCGA	CCGGGACGGA	GCGCCCGCCA	240
GTCCCAGGTG	GCCCGGACCG	CACGTTGCGT	CCCCGCGCTC	CCCGCCGGCG	ACAGGAGACG	300
CTCCCCCCA	CGCCGCGCGC	GCCTCGGCCC	GGTCGCTGGC	CCGCCTCCAC	TCCGGGGACA	360
AACTTTTCCC	GAAGCCGATC	CCAGCCCTCG	GACCCAAACT	TGTCGCGCGT	CGCCTTCGCC	420

GGGAGCCGTC CGCGCAGAGC GTGCACTTCT CGGGCGAG ATG TCG GAG CGC AGA GAA 476 Met Ser Glu Arg Arg Glu 1 5
GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG
AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA GCC TTG CCT CGC CGC 572 Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala Leu Pro Pro Arg 25 30 35
TTG AAA GAG ATG AAG ATG CAG GAG TCT GTG GCA GGT TCC AAA CTA GTG 620 Leu Lys Glu Met Lys Met Gln Glu Ser Val Ala Gly Ser Lys Leu Val 40 45 50
CTT CGG TGC GAG ACC AGT TCT GAA TAC TCC TCT CTC AAG TTC AAG TGG 668 Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys Trp 55 60 65 70
TTC AAG AAT GGG AGT GAA TTA AGC CGA AAG AAC AAA CCA CAA AAC ATC 716 Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys Pro Gln Asn Ile 75 80 85
AAG ATA CAG AAA AGG CCG GGG AAG TCA GAA CTT CGC ATT AGC AAA GCG 764 Lys Ile Gln Lys Arg Pro Gly Lys Ser Glu Lev Arg Ile Ser Lys Ala 90 95 100
TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA 812 Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu 105 110 115
GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GAG 860 Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Glu 120 125 130
ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT TCA 908 Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser Ser 135 140 145 150
GAG TCT CCC ATT AGA ATA TCA CTA TCA ACA GAA GGA ACA AAT ACT TCT 956 Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr Ser 155 160 165
TCA TCC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG TGT 1004 Ser Ser Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys Cys 170 175 180
GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC ATG 1052 Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met 185 190 195
GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG TGC AAG TGC CCA AAT 1100 Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn 200 205 210
GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC 1148 Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr 215 220 225 230
AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAGGCGCATG CTCAGTCGGT 1201 Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu 235 240
GCCGCTTTCT TGTTGCCGCA TCTCCCCTCA GATTCAACCT AGAGCTAGAT GCGTTTTACC 1261

AGGTCTAACA TTGACTGCCT CTGCCTGTCG CATGAGAACA TTAACACAAG CGATTGTATG 1321 ACTTCCTCTG TCCGTGACTA GTGGGCTCTG AGCTACTCGT AGGTGCGTAA GGCTCCAGTG 1381 TTTCTGAAAT TGATCTTGAA TTACTGTGAT ACGACATGAT AGTCCCTCTC ACCCAGTGCA 1441 ATGACAATAA AGGCCTTGAA AAGTCTCACT TTTATTGAGA AAATAAAAAAT CGTTCCACGG 1501 ACCAGTACAC ACTTGAAATG ATGGTAAGTT CGCTTCGGTT CAGAATGTGTA 1561 AAATAAACAG AATAAAAAAA AAAAAAAAAA A
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 149.
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1140 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:
CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG 48 His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu 1 5 10 15
CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TGC 96 Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys 20 25 30
GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG 144 Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu 35 40 45
GCC AAC AGC AGC GGC GGG CCC GGC CTT CCG AGC CTC CTT CCC CCC 192 Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro 50 55 60
TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG 240 Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val 65 70 75 80
CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG 288 Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu 85 90 95
TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA 336 Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu 100 105 110
TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC 384 Tyr Ser Ser Len Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser 115 120 125
CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG 432 Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys 130 135 140
TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT 480 Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr 145 150 155 160
ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC 528 Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn 165 170 175
ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA 576

Ile	Thr	Ile	Val 180	Glu	Ser	Asn	Ala	Thr 185	Ser	Thr	Ser	Thr	Ala 190	Gly	Thr	
AGC Ser	CAT His	CTT Leu 195	GTC Val	AAG Lys	TGT Cys	GCA Ala	GAG Glu 200	AAG Lys	GAG Glu	AAA Lys	ACT Thr	TTC Phe 205	TGT Cys	GTG' Va'l	AAT Asn	624
GGA Gly	GGC Gly 210	GAG Glu	TGC Cys	TTC Phe	ATG Met	GTG Val 215	AAA Lys	GAC Asp	CTT Leu	TCA Ser	AAT Asn 220	CCC Pro	TCA Ser	AGA Arg	TAC Tyr	672
TTG Leu 225	TGC Cys	AAG Lys	TGC Cys	CAA Gln	CCT Pro 230	GGA Gly	TTC Phe	ACT Thr	GGA Gly	GCG Ala 235	AGA Arg	TOT Cys	ACT Thr	GAG Glu	AAT Asn 240	720
GTG Val	CCC Pro	ATG Met	AAA Lys	GTC Val 245	CAA Gln	ACC Thr	CAA Gln	GAA Glu	AAG Lys 250	TGC Cys	c¢A Pro	AAT Asn	GAG Glu	TTT Phe 255	ACT Thr	768
GGT Gly	GAT Asp	CGC Arg	TGC Cys 260	CAA Gln	AAC Asn	TAC Tyr	GTA Val	ATG Met 265	Ala	XGC Ser	TTC Phe	TAC Tyr	AGT Ser 270	ACG Thr	TCC Ser	816
ACT Thr	CCC Pro	TTT Phe 275	CTG Leu	TCT Ser	CTG Leu	CCT Pro	GAA Glu 280	TAG	CCCA'	rct (CAGT	CGGT	GC C	GCTT	TCTT	G 870
TTG	CCGC	ATC	TCCC	CTCA	GA T	rccn(CCTA	g /AG	CTAG	ATGC	GTT	TTAC	ÇAG (GTCT	AACA	TT 930
GAC	TGCC'	гст	GCCT	GTCG	CA T	GAGA	ACAT	T AA	CACA	AGCG	ATT	GTAT	GAC	TTCC	TCTG	TC 990
CGT	GACT	AGT	GGGC	TCTG.	AG C'	TACT	CG7A	G GT	GCGT.	AAGG	CTC	CAGT	GTT	TCTG	AAAT	TG 1050
ATC	TTGA	ATT .	ACTG	TGAT.	AC G	ACAT	ЭАТА	G TC	CCTC	TCAC	CCA	GTGC	AAT	GACA	ATAA	AG 1110
	TTGA.					/	<i>'</i>									1140
(2)					/				FICA	TION	NUM	BER:		150:		
	(i)	SEQ	UENC	E CH	ARAC	TERI	STIC	S:								
		(B) LE) TY) ST	PE:/	EDNE	SS:		n	764 ucle ingl		cid					
		(D) Т9	POLO	GY:			1	inea	r						
	(xi) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	0: 1	50:					
G A	AG T ys S 1	CA G er G	/ AA C lu L	TT C eu A	GC A rg I 5	TT A le S	GC A er L	AA G ys A	la S	CA C er L 10	TG G eu A	CT G la A	AT T	CT G er G	GA G ly G 15	AA 49 lu
TAT Tyr	ATG Met	TGC Cys	AAA Lys 20	. GTG Val	ATC Ile	AGC Ser	AAA Lys	CTA Leu 25	GGA Gly	AAT Asn	GAC Asp	AGT Ser	GCC Ala 30	TCT Ser	GCC Ala	97
	ATC Ile															
ACA	AGC	CAT	CTI	GTC	AAG	TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	193

															/		
Thr	Ser 50	His	Leu	Val	Lys	Cys 55	Ala	Glu	Lys	Glu	Lys 60	Thr	Phe	CAa	Val		
AAT Asn 65	GGA Gly	GGC Gly	GAC Asp	TGC Cys	TTC Phe 70	ATG Met	GTG Val	AAA Lys	GAC Asp	CTT Leu 75	TCA Ser	AAT Asn	CCC Pro	TCA Ser	AGA Arg 80	241	
TAC Tyr	TTG Leu	TGC Cys	AAG Lys	TGC Cys 85	CAA Gln	CCT Pro	GGA Gly	TTC Phe	ACT Thr 90	GGA Gly	GCG Ala	AGA Arg/	TGT Cys	ACT Thr 95	GAG Glu	289	
AAT Asn	GTG Val	CCC Pro	ATG Met 100	AAA Lys	GTC Val	CAA Gln	Thr	CAA Gln 105	GAA Glu	AAA Lys	GCG Ala	GIu/	GAG Glu 110	CTC Leu	TAC Tyr	337	
CAG Gln	AAG Lys	AGA Arg 115	GTG Val	CTC Leu	ACC Thr	ATT Ile	ACC Thr 120	GGC Gly	ATT Ile	TGC Cys	ATC Ile	GCG Ala 125	CTG Leu	CTC Leu	GTG Val	385	
GTT Val	GGC Gly 130	ATC Ile	ATG Met	TGT Cys	GTG Val	GTG Val 135	GTC Val	TAC Tyr	TGC Cys	AAA Lys	ACC Thr 140	AAG Lys	AAA Lys	CAA Gln	CGG Arg	433	
AAA Lys 145	AAG Lys	CTT Leu	CAT His	GAC Asp	CGG Arg 150	CTT Leu	CGG Arg	CAG Gln	AGC Ser	CTT Leu 155	CGG Arg	TCT Ser	GAA Glu	AGA Arg	AAC Asn 160	481	
ACC Thr	ATG Met	ATG Met	AAC Asn	GTA Val 165	GCC Ala	AAC Asn	GGG Gly	coc Pro	CAC His 170	CAC His	CCC Pro	AAT Asn	CCG Pro	CCC Pro 175	CCC Pro	529	
GAG Glu	AAC Asn	GTG Val	CAG Gln 180	CTG Leu	GTG Val	AAT Asn	CAA Oʻln	TAC Tyr 185	GTA Val	TCT Ser	AAA Lys	AAT Asn	GTC Val 190	ATC Ile	TCT Ser	577	
AGC Ser	GAG Glu	CAT His 195	ATT Ile	GTT Val	GAG Glu	aga arg	GAG Glu 200	GCG Ala	GAG Glu	AGC Ser	TCT Ser	TTT Phe 205	TCC Ser	ACC Thr	AGT Ser	625	
CAC His	TAC Tyr 210	ACT Thr	TCG Ser	ACA Thr	GCT Ala	CAT His 215	CAT His	TCC Ser	ACT Thr	ACT Thr	GTC Val 220	ACT Thr	CAG Gln	ACT Thr	CCC Pro	673	
AGT Ser 225	CAC His	AGC Ser	TGG Trp	AGC Ser	AAT Asn 230	GGA Gly	CAC His	ACT Thr	GAA Glu	AGC Ser 235	ATC Ile	ATT Ile	TCG Ser	GAA Glu	AGC Ser 240	721	
					Met	TCA Ser				Asn						769	
						GGA Gly									CGT Arg	817	
			Ser			AGG Arg									TAC Tyr	865	
		Ser													AGG Arg	913	
AGA	AAC	AAG	GCC	CAC	AGA	TCC	AAA	TGC	ATG	CAG	ATC	CAG	CTT	TCC	GCA	961	

	Arg 305	Asn	Lys	Ala	His	Arg 310	Ser	Lys	Cys	Met	Gln 315	Ile	Gln	Leu	Ser	Alá 320	
	ACT Thr	CAT His	CTT Leu	AGA Arg	GCT Ala 325	TCT Ser	TCC Ser	ATT Ile	CCC Pro	CAT His 330	TGG Trp	GCT Ala	TCA Ser	TTC Phe	TCT Ser 335	AAG Lys	1009
	ACC Thr	CCT Pro	TGG Trp	CCT Pro 340	TTA Leu	GGA Gly	AGG Arg	TAT Tyr	GTA Val 345	TCA Ser	GCA Ala	ATG Met	ACC Thr	ACC Thr 350	CCG Pro	GCT Ala	1057
	CGT Arg	ATG Met	TCA Ser 355	CCT Pro	GTA Val	GAT Asp	TTC Phe	CAC His 360	ACG Thr	CCA Pro	AGC Ser	TCC Ser	Pro 365	AAG Lys	TCA Ser	CCC Pro	1105
	CCT Pro	TCG Ser 370	GAA Glu	ATG Met	TCC Ser	CCG Pro	CCC Pro 375	GTG Val	TCC Ser	AGC Ser	ACG Thr	ACG Thr 380	GTC Val	TCC Ser	ATG Met	CCC Pro	1153
	TCC Ser 385	ATG Met	GCG Ala	GTC Val	AGT Ser	CCC Pro 390	TTC Phe	GTG Val	GAA Glu	GAG Gla	GAG Glu 395	AGA Arg	CCC Pro	CTG Leu	CTC Leu	CTT Leu 400	1201
	GTG Val	ACG Thr	CCA Pro	CCA Pro	CGG Arg 405	CTG Leu	CGG Arg	GAG Glu	AAG Lys	TAT Tyr 410	GAC Asp	CAC His	CAC His	GCC Ala	CAG Gln 415	CAA Gln	1249
	TTC Phe	AAC Asn	TCG Ser	TTC Phe 420	CAC His	TGC Cys	AAC Asn	CCC/ Pro	GCG Ala 425	CAT His	GAG Glu	AGC Ser	AAC Asn	AGC Ser 430	CTG Leu	CCC Pro	1297
	CCC Pro	AGC Ser	CCC Pro 435	TTG Leu	AGG Arg	ATA Ile	GTO Va(1	GAG Glu 440	GAT Asp	GAG Glu	GAA Glu	TAT Tyr	GAA Glu 445	ACG Thr	ACC Thr	CAG Gln	1345
	GAG Glu	TAC Tyr 450	GAA Glu	CCA Pro	GCT Ala	CAX GYn	GAG Glu 455	CCG Pro	GTT Val	AAG Lys	AAA Lys	CTC Leu 460	ACC Thr	AAC Asn	AGC Ser	AGC Ser	1393
	CGG Arg 465	CGG Arg	GCC Ala	AAA Lys	AGA Azg	ACC Thr 470	AAG Lys	CCC Pro	AAT Asn	GGT Gly	CAC His 475	ATT Ile	GCC Ala	CAC His	AGG Arg	TTG Leu 480	1441
	GAA Glu	ATG Met	GAC Asp	AA¢ Asn	AAC Asn 485	ACA Thr	GGC Gly	GCT Ala	GAC Asp	AGC Ser 490	AGT Ser	AAC Asn	TCA Ser	GAG Glu	AGC Ser 495	GAA Glu	1489
	ACA Thr	GAG Glu	GAT Asp	GAA Glu 500	AGA Arg	GTA Val	GGA Gly	GAA Glu	GAT Asp 505	ACG Thr	CCT Pro	TTC Phe	CTG Leu	GCC Ala 510	ATA Ile	CAG Gln	1537
				Ala	GCC Ala				Ala								1585
	GAC Asp	AGC Ser 530	Arg	ACT Thr	AAC Asn	CCA Pro	ACA Thr 535	GGC Gly	GGC Gly	TTC Phe	TCT Ser	CCG Pro 540	Gln	GAA Glu	GAA Glu	TTG Leu	1633
/		Ala			TCC Ser							Asp					1681
	TAA	AACC	GAA	ATAC	ACCC.	AT A	GATT	CACC	T GT	AAAA	CTTT	ATT	TTAT	ATA	ATAA	AGTATT	1741

CCACCTTAAA TTAAACAAAA AAA (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 151: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: amino acid (B) TYPE: (C) STRANDEDNESS: linear (D) TOPOLOGY: ` (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151: Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys 10 Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys 20 Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln/Asn Tyr Val Met Ala Ser 40 Phe Tyr 50 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 152: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 amino acid (B) TYPE: (C) STRANDEDNESS (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152: Lys Cys Ala Glu Lys G/Lu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys 20 Gln Pro Gly Phe/Thr Gly Ala Arg Cys Thr Glu Asn Val Pro Met Lys Val Gln 50 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 153: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 amino acid (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

 $\operatorname{Gl}\psi$ Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His Gly Glu Cys Lys

T√r Val Lys Glu Leu Arg Ala Pro Ser Cys Lys Cys Gln Gln Glu Tyr

155

Phe Gly Glu Arg Cys Gly Glu Lys Ser Asn Lys Thr His Ser 35 40 45

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:

154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:

198

(B) TYPE:

nucleic acid

(C) STRANDEDNESS:
(D) TOPOLOGY:

single linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn 1 5 10 15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
20 25/ 30

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC 144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
35 40 45

GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT 192
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro
50 60

GAA TAG

198

Glu 65

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 155:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

192

(B) TYPE:

nucleic acid

(C) STRANDEDNESS:

singre

(D) TØPOLOGY:

linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:
- AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn 1 5 10

GGA GGC/GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
20 25 30

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
35
40
45

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC TAA 192 yal Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr

156:

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: (B) TYPE:

183 nucleic acid

(C) STRANDEDNESS

single

(D) TOPOLOGY:

linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48 Ser His Leu Val Lys Cys Ala\Glu Lys Glu Lys Thr Phe Cys Val Asn

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96 Gly Glu Cys Phe Met Val Tys Asp Leu Ser Asn Pro Ser Arg Tyr 25 2.0

TTG TGC AAG TGC CCA AAT GAG TYT ACT GGT GAT CGC TGC CAA AAC TAC 144 Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr 40

GTA ATG GCC AGC TTC TAC AAA GCG GAG GAG CTC TAC TAA Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr 55

157:

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

210

(B) TYPE:

nucleic acid

(C) STRANDEDNESS:

single

(D) TOPOLOGY:

linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO ₹ 157:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96 Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser\Asn Pro Ser Arg Tyr

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC 144 Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr 40

GTA ATG GCC AGC TTC TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG AAA 192 Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Gaturalu Phe Met Glu Lys 55 60

GCG GAG GAG CTC TAC TAA

210

Ala Glu Glu Leu Tyr

(i) SEQUENCE CHARACTERISTICS: 267 (A) LENGTH nucleic acid (B) TYPE: (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158: AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96 Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr 25 TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144 Leu Cys Lys Cys Gln Pro Gl\/y Phe Thr Gly Ala Arg Cys Thr Glu Asn 40 GTG CCC ATG AAA GTC CAA ACC\CAA GAA AAG TGC CCA AAT GAG TTT ACT 192 Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr 55 GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC 240 Gly Asp Arg Cys Gln Asn Tyr Vall Met Ala Ser Phe Tyr Ser Thr Ser ACT CCC TTT CTG TCT CTG CCT GAA\TAG 267 Thr Pro Phe Leu Ser Leu Pro Glu 85 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 159: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: lidear (xi) SEQUENCE DESCRIPTION: SEQ ID \NO: 159: AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96 Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr 20 25 30 TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144 Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGQ CCA AAT GAG TTT ACT 192

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:

Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr 50 60
GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AAA GCG GAG 240 Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu 65 70 80
GAG CTC TAC TAA Glu Leu Tyr
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 160:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:
CC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG TGT GCA Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys Cys Ala 1 5 10 15
GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC ATG GTG 95 Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val 20 30
AAA GAC CTT TCA AAT CCC TCA AGA TAC Leu Lys Asp Leu Ser Asn Pro Ser Arg Tyr 35 40 128
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 161:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:
A CAT AAC CTT ATA GCT GAG CTA AGG AGA AAC AAG GCC CAC AGA TCC His Asn Leu Ile Ala Glu Leu Arg Arg Asn Lys Ala His Arg Ser 1 5 10 15
AAA TGC ATG CAG ATC CAG CTT TCC GCA ACT CAT CTT AGA GCT TCT TCC 94 Lys Cys Met Gln Ile Gln Leu Ser Ala Thr His Leu Arg Ala Ser Ser 20 25 30
ATT CCC CAT TGG GCT TCA TTC TCT AAG ACC CCT TGG CCT TTA GGA AG Ile Pro His Trp Ala Ser Phe Ser Lys Thr Pro Trp Pro Leu Gly Arg 35 45
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 162:
(i) SEQUENCE CHARACTERISTICS:

```
(A) LENGTH:
                                 24
         (B) TYPE:
                                 amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY:
                                 /linear
    (ix) FEATURE:
         (D) OTHER INFORMATION: / Xaa in positions 15 and 22 is
unknown.
    (xi) SEQUENCE DESCRIPTION: $EQ ID NO: 162:
Ala Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Xaa Phe
                                     10
Met Val Lys Asp Leu Xaa Asn P‡o
            20
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:
                                                       163:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH:
                                  nucleic acid
         (B) TYPE:
         (C) STRANDEDNESS
                                  single
         (D) TOPOLOGY:
                                  linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:
ATG AGA TGG CGA CGC GCC CGC CGC TCC GGG CGT CCC GGC CCC CGG 48
Met Arg Trp Arg Arg Ala/Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg
GCC CAG CGC CCC GGC TCQ GCC CGC TCG TCG CCG CCG CTG CCG CTG 96
Ala Gln Arg Pro Gly Set Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu
CTG CCA CTA CTG CTG CTG GGG ACC GCG GCC CTG GCG CCG GGG GCG 144
Leu Pro Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
GCG GCC GGC AAC GAG GCG GCT CCC GCG GGG GCC TCG GTG TGC TAC TCG 192
Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
TCC CCG CCC AGC GTG/GGA TCG GTG CAG GAG CTA GCT CAG CGC GCC GCG 240
Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala
GTG GTG ATC GAG GGA AAG GTG CAC CCG CAG CGG CGG CAG CAG GGG GCA 288
Val Val Ile Glu GÁy Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala
CTC GAC AGG AAG GCG GCG GCG GCG GGC GAG GCA GGG GCG TGG GGC 336
Leu Asp Arg Lys/Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly
            100/
                               105
GGC GAT CGC GAG CCG CCA GCC GCG GGC CCA CGG GCG CTG GGG CCG CCC 384
Gly Asp Arg G/u Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro
        115
```

GCC GAG GAG CCG CTG CTC GCC GCC AAC GGG ACC GTG CCC TCT TGG CCC 432 Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro 135 ACC GCC CCG GTG CCC AGC GCC GGC GAG GAG GAG GCG CCC TAT 480 Thr Ala Pro Val Pro Ser Ala Gly Glu\Pro Gly Glu Glu Ala Pro Tyr 155 150 CTG GTG AAG GTG CAC CAG GTG TGG GCG GTG AAA GCC GGG GGC TTG AAG 528 Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys AAG GAC TCG CTG CTC ACC GTG CGC CTG GGG ACC TGG GGC CAC CCC GCC 576 Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala 185 TTC CCC TCC TGC GGG AGG CTC AAG GAG GAQ AGC AGG TAC ATC TTC TTC 624 Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe 200 195 Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg 215 220 210 GCC TCT TTC CCC CCT CTG GAG ACG GGC CGG AAC CTC AAG AAG GAG GTC 720 Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Ash Leu Lys Lys Glu Val 235 230 225 745 AGC CGG GTG CTG TGC AAG CGG TGC G Ser Arg Val Leu Cys Lys Arg Cys 245 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: (i) SEOUENCE CHARACTERISTICS: 12 (A) LENGTH: amino acid (B) TYPE: (C) STRANDEDNESS: linear (D) TOPOLOGY: (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is unknown. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164: Xaa Ala Leu Ala Ala Ala Gly Tyr Asp Val Glu Lys (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 165: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is unknown.

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:
Xaa 1	Leu Val Leu Arg
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 166:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 11 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear
	(ix) FEATURE:
unkı	(D) OTHER INFORMATION: Xa in positions 1, 2, and 3 is nown.
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:
Xaa 1	Xaa Xaa Tyr Pro Gly Gln Ile Thr Ser Asn 5 10
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 167:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 60 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
	(ix) FEATURE:
	(D) OTHER INFORMATION: N in positions 25 and 36 is unknown.
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:
ATA	GGGAAGG GCGGGGGAAG GGTCNCCCTC NGCAGGGCCG GGCTTGCCTC TGGAGCCTCT 60
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 168:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 18 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
	(ix) FEATURE
	(D) OTHER INFORMATION: N in position 16 is unknown.
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:
TTT	ACACATA TATCCNCC 18
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:

21

(B) TYPE:

amino açid

- (C) STRANDEDNESS:
- (D) TOPOLOGY:

linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:
- Glu Thr Gln Pro Asp Pro Gly Gln Ile Leu Lys Lys Val Pro Met Val

Ile Gly Ala Tyr Thr

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 170:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:

422

(B) TYPE:

- amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY:

- linear
- (xi) SEQUENCE DESCRIPT ON: SEQ ID NO: 170:
- Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg

 1 10 15
- Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu 20 25 30
- Leu Pro Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
 35 40 45
- Ala Ala Gly Asn Gly Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
 50 55 60
- Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala 65 70 75 80
- Val Val Ile Gly Cly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala 85 90 95
- Leu Asp Arg Lys Ala Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly
 100 105 110
- Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro 1/5 120 125
- Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro
- Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr
 145 150 155 160
- Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys
- Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala 180 185 190
- The Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe 195 200 205

Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala/Ala Phe Arg Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val 235 Ser Arg Val Leu Cys Lys Arg Cys Ala Leu Pro Pro Gln Leu Lys Glu 250 Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys/Leu Val Leu Arg Cys 265 Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn 280 Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro/Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg Lie Asn Lys Ala Ser Leu Ala 315 Asp Ser Gly Glu Tyr Met Cys Lys Val/Ile Ser Lys Leu Gly Asn Asp 330 Ser Ala Ser Ala Asn Ile Thr Ile Vall Glu Ser Asn Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Nal Lys Cys Ala Glu Lys Glu Lys 360 Thr Phe Cys Val Asn Gly Gly Glp Cys Phe Met Val Lys Asp Leu Ser 375 Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp 395 390 385 Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro 410 405 Phe Leu Ser Leu Pro Glu 420

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 171:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:

69

(B) TYPE:

amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

linear

(xi) SEQUENCE/DESCRIPTION: SEQ ID NO: 171:

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Lys Lys 1 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser

Pro Arg Glu Tle Ile Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr

Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala

60

50

Asn Thr Ser Ser Ser 65

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 172:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

19

(B) TYPE:

amino aci¢

(C) STRANDEDNESS: (D) TOPOLOGY:

linear

172: (xi) SEQUENCE DESCRIPTION: SEQ ID NO;

Arg Lys Gly Asp Val Pro Gly Pro Arg Val/Lys Ser Ser Arg Ser Thr

Thr Thr Ala

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

231

(B) TYPE:

nucleic acid

(C) STRANDEDNESS:

single linear

(D) TOPOLOGY:

(xi) SEQUENCE DESCRIPTION / SEQ ID NO: 173:

CGCGAGCGCC TCAGCGCGGC CGCTCG&TCT CCCCCTCGAG GGACAAACTT TTCCCAAACC 60 CGATCCGAGC CCTTGGACCA AACTCGCCTG CGCCGAGAGC CGTCCGCGTA GAGCGCTCCG 120 TCTCCGGCGA GATGTCCGAG CGCÁAAGAAG GCAGAGGCAA AGGGAAGGGC AAGAAGAAGG 180 AGCGAGGCTC CGGCAAGAAG CØGGAGTCCG CGGCGGGCAG CCAGAGCCCA G 231

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 174:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE/

178 nucleic acid

(C) STRANDEDNESS:

single

(D) TOPOLOGY:

linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

CCTTGCCTCC C¢GATTGAAA GAGATGAAAA GCCAGGAATC GGCTGCAGGT TCCAAACTAG 60 TCCTTCGGTG /TGAAACCAGT TCTGAATACT CCTCTCTCAG ATTCAAGTGG TTCAAGAATG 120 GGAATGAAT√ GAATCGAAAA AACAAACCAC AAAATATCAA GATACAAAAA AAGCCAGG

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 175:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	122 nucleic acid single linear		
(xi)	SEQUENCE DESCRIPTION: SE	EQ ID NO: 175:/		
GAAGTCAGA	AA CTTCGCATTA ACAAAGCATC	ACTGGCTGAT TCTGGAGAGT	ATATGTGCAA	60
AGTGATCAC	GC AAATTAGGAA ATGACAGTGC	CTCTGCCAAT ATCACCATCG	TGGAATCAAA	120
CG				122
(2) INFO	RMATION FOR SEQUENCE IDEN	NTIFICATION NUMBER:	176:	
(i) s	SEQUENCE CHARACTERISTICS	:		
	(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	102 / nucleic acid single linear		
(xi)	SEQUENCE DESCRIPTION: SI	EQ/ID NO: 176:		
AGATCATC	AC TGGTATGCCA GCCTCAACTG	AAGGAGCATA TGTGTCTTCA	GAGTCTCCCA	60
TTAGAATA'	TC AGTATCCACA GAAGGAGCAA	ATACTTCTTC AT	:	102
(2) INFO	RMATION FOR SEQUENCE IDE	NTIFICATION NUMBER:	177:	
· (i) :	SEQUENCE CHARACTERISTICS	:		
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	128 nucleic acid single linear		
(xi)	SEQUENCE DESCRIPTION: S	EQ ID NO: 177:		
CTACATCT	AC ATCCACCACT GEGACAAGCC	ATCTTGTAAA ATGTGCGGAG	AAGGAGAAAA	60
CTTTCTGT	GT GAATGGAGGG GAGTGCTTCA	TGGTGAAAGA CCTTTCAAAC	CCCTCGAGAT	120
ACTTGTGC				128
(2) INFO	RMATION FOR SEQUENCE IDE	NTIFICATION NUMBER:	178:	
(i)	SEQUENCE CHARACTERISTICS	:		
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	69 nucleic acid single linear		
(xi)	SEQUENCE DESCRIPTION: S	EQ ID NO: 178:		
AAGTGCCA	AC CTGGATTCAC TGGAGCAAGA	TGTACTGAGA ATGTGCCCAT	GAAAGTCCAA	60
AACCAAGA	A /			69
(2) INFO	RMATION FOR SEQUENCE IDE	NTIFICATION NUMBER:	179:	

,		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: 23 nucleic acid single linear		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179: $/$		
TCGGGCTCCA TGAAGAAGAT GTA		23
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:	180:	
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 23 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear		
(xi) SEQUENCE DESCRIPTION: SEQ IN NO: 180:		
TCCATGAAGA AGATGTACCT GCT		23
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:	181:	
(i) SEQUENCE CHARACTERISTICS		
(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: 22 nucleic acid single linear		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:		
ATGTACCTGC TGTCCTCCTT GA		22
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:	182:	
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: (B) TYPE: nucleic acid (C) STRANDEDWESS: single (D) TOPOLOGY: linear		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:		
TTGAAGAAGG ACTCGCTGCT CA		22
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:	183:	
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 20 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:		

(2)	INFORMATION FOR SEQUENCE IDEN	rification number	184:	
	(i) SEQUENCE CHARACTERISTICS:			
	(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	nucleic acid single linear		
	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 184:		
ATGA	RGTGTG GGCGGCGAAA			20
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	185:	
	(i) SEQUENCE CHARACTERISTICS:			
	(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	15 amino acid linear		
	(xi) SEQUENCE DESCRIPTION: SE	Q Ip NO: 185:		
Glu	Gly Lys Val His Pro Gln Arg A 5	rg/Gly Ala Leu Asp	Arg Lys	
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	186:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	17 amino acid linear		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:			
Pro	Ser Cys Gly Arg Leu Lys Glu A	sp Ser Arg Tyr Ile 10	Phe Phe 15	Met Glu
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:		187:	
	(i) SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	16 amino acid linear		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:			
Glu	Leu Asn Arg Lys Asn Lys Pro G	In Asn Ile Lys Ile 10	Gln Lys 15	Lys
(2)	INFORMATION FOR SEQ ID NO:188):		
	(i) SEQUENCE CHARACTERISTI	CCS:		

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Cys Thr Ala Cys Ala Thr Cys Thr Ala Cys Ala Thr Cys Cys Ala Cys Cys Cys Ala Thr Cys Ala Cys Thr Gly Gly Gly Ala Cys Ala Ala Gly 25 20 Cys Thr Thr Gly Thr Ala Ala Ala Ala Thr Gly Thr Gly Cys Gly Gly Ala Gly Ala Ala Gly Gly Ala Gly Ala Ala Ala Ala Cys Thr Thr Thr Cys Thr Gly Thr Gly Thr Gly Ala Ala Thr Gly Gly Ala Gly Gly 70 Gly Ala Gly Thr Gly Cys Thr Thr Cys Ala Thr Gly Gly Thr Gly Ala 90 85 Ala Ala Gly Ala Cys Cys Thr Thr Thr Cys/Ala Ala Ala Cys Cys Cys 110 105 100 Cys Thr Cys Gly Ala Gly Ala Thr Ala Cys Thr Thr Gly Thr Gly Cys 125 120 Thr Cys Gly Gly Cys Thr Cys Cys Ala Thr Gly Ala Ala Gly Ala 135 140 130 Ala Gly Ala Thr Gly Thr Ala

- (2) INFORMATION FOR SEQ ID NO:189:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 211 amino adids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: sing/e
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Cys Thr Ala Cys Ala Thr C/s Thr Ala Cys Ala Thr Cys Cys Ala Cys Cys Ala Cys Thr Gly Gly Ala Cys Ala Ala Gly Cys Cys Ala Thr 25 20 Cys Thr Thr Gly Thr Ala Ala Ala Thr Gly Thr Gly Cys Gly Gly Ala Gly Ala Ala Gly G/1y Ala Gly Ala Ala Ala Cys Thr Thr Thr Cys Thr Gly Thr Gly/Thr Gly Ala Ala Thr Gly Gly Ala Gly Gly Gly Gly Ala Gly Thr Gly Cys Thr Thr Cys Ala Thr Gly Gly Thr Gly Ala 90 Ala Ala Gly Ala Cys Cys Thr Thr Thr Cys Ala Ala Ala Cys Cys Cys 100 105 110 Cys Thr Cys Gly Ala Gly Ala Thr Ala Cys Thr Thr Gly Thr Gly Cys 120 Ala Ala Gly Thr Gly Cys Cys Cys Ala Ala Ala Thr Gly Ala Gly Thr 135 Thr Thr Ala Cy/s Thr Gly Gly Thr Gly Ala Thr Cys Gly Cys Thr Gly 150 155 Cys Cys Ala Ala Ala Ala Cys Thr Ala Cys Gly Thr Ala Ala Thr Gly 165 170 Gly Cys Cys Ala Gly Cys Thr Thr Cys Thr Ala Cys Thr Cys Cys Ala Thr Gly Ala Ala Gly Ala Ala Gly Ala Thr Gly Thr Ala Cys Cys Thr 195 200 200 205